

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 111490

TO: Mark Navarro Location: cm1/8a15

Art Unit: 1645

Tuesday, January 06, 2004

Case Serial Number: 08/482785

From: Barb O'Bryen

Location: Biotech-Chem Library

CM1-6A05

Phone: 308-4291

barbara.obryen@uspto.gov

Search Notes

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Result
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Listing first 45 summaries
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S. pyogenes DNase
DNA-ase-B2 N-termi
                                                                                                                                                                                                                            Description
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                                            DNA-ase-B.
DNA-ase-B. Strept
Interferon induced
Human liver peptid
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Plasmid pBTA732-en Plasmid pBTA735-en	lasmid pBTA730-e	lasmid pBTA731-e	emid pBTA733-e	smid pBTA734-e	DBTA609	ie excret	uman die	erium	nila melan	8	Cps2A protein invo	n which	1 Pol 1	uman di	ollen Al	sophila	pneum	ollen A	6	length Amb	rge	weed	a I/Antigen E	eed allerger	of Amb a	man peptide enc	ide #4620 enc	eptide #4856	ide #4765	bone marro	an brain expre	tein #4653 enc	ptide #4871 enc	de #47

ALIGNMENTS

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RESULT 1
AAR88822
                   PT PT XXXX PXXXX PXXX PXXXX PXXX PXXXX PXXX PXXXX PXXX PXXX
New DNA encoding Streptococcus pyogenes DNase B - prodn. of the enzyme in other bacteria, useful in for treating cystic fibrosis
                                                                                                                                                                                                    WPI; 1996-151377/15.
                                                                                                                                                                                                                                                                                       Adams CW, Belei MC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNase B; nuclease; cystic fibrosis; vaccine; immunoassay; diagnosis; leader peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR88822;
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RESULT 2
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Matches 43
                             A partial sequence (AAR88821) for Streptococcus pyogenes DNase B is the product of DNA clone lambda 2-6 (AAR12773) isolated from a spyogenes DNA library. A full-length sequence is given in AAR88823. The insert of the DNase B-encoding DNA clone can be transferred to expression plasmids for large-scale recombinant DNase produ. in E. coli or other bacterial hosts. It is used in immunoassays to detect anti-DNase B antibodies in serum as a marker of S: pyogenes infection, and is also useful as a vaccine
                                                                                                                                                  Example 2; Fig 3; 115pp; English.
                                                                                                                                                                                         New DNA encoding Streptococcus pyogenes DNase B - prodn. of the enzyme in other bacteria, useful in
                                                                                                                                                                                                                                                WPI; 1996-151377/15.
                                                                                                                                                                                                                                                                           Adams CW,
                                                                                                                                                                                                                                                                                                                              18-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can be used to facilitate prodn. of recombinant DNase B (see AAR8823) in transformed bacterial hosts, e.g. Escherichia co The leader peptide can also be used for expression and prodn of other recombinant proteins in bacteria. The product is excreted by the host into the culture medium and is easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 89; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recovered
                 rker of S. pyogenes infection, and is also useful as a vaccine for cystic fibrosis treatment via aerosol delivery.
                                                                                                                                                                               treating cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nuclease; cystic fibrosis; vaccine;
s; Escherichia coli.
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sed to facilitate prodn. of recombinant DNase B (see
                                                                                                                                                                                                                                                                         Belei MC,
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Pred. No. 1.5e-23;
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Sequence

RESULT 4
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ID AAR5
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AC AAR5
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DT 25-M
DT 29-M

AAR58702 standard;

Protein;

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25-MAR-2003 29-MAR-1995 AAR58702;

(updated)
(first entry)

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RESULT 3
AAR70700
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Best Local
                                                                                                                                                                                                                                                                The sequence represents the N-terminal fragment of Streptococcus pyogenes DNA-ase-B, which is a marker of S. pyogenes infection. The protein may be used as a diagnostic agent or vaccine for S. pyogenes, or may be used as an aerosol to treat excessive lung viscosity, e.g. in cystic fibrosis.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Fig 3; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding Streptococcus pyogenes DNase B - for diagnosing S. pyogenes infection, also new promoter for expressing other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ85036
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14-AUG-1995
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                                                                                                                                                                                                                        91 AA;
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-US05626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0082845
                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pang PPY;
                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                   Score 203; DB 16;
Pred. No. 3.7e-23;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 203; DB 17;
Pred. No. 3.6e-23;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic; vaccine; cystic
                                                                                                      Indels
                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
43
                                                                                                                                                         91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
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                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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ARRUBLY 5
AARRUBLY 5
AARRUBLY 5
AARRUBLY 25-J
XX AARRUBLY 25-J
XX DNAB
XX DNAB
XX DNAB
XX DNAB
XX CIAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR58702 shows a mitogenic factor which exhibits rabbit peripheral blood lymphocyte mitogenicity and/or DNA hydrolysing activity. It is strongly associated with group A Streptocaci and the nucleotide sequences can be used for the microdetection of the gene and provide an early diagnosis of infectious disease caused by the bacteria. (See also AAQ71613-26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mitogenic factor gene from Streptococcus pyogenes - used develop prods. for the early diagnosis of infectious disease caused by gp A streptococci
                                                                       Protein
                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                     S. pyogenes DNaseB and leader sequence
                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1996
WO9606174-A1
                                                                                                                                                                                                                                             diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                      AAR88823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR88823 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1994
                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 12-13; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP613947-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  delayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erythrogenic toxin; streptococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitogenic factor; microdetection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitogenic factor associated with group A Streptococci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fever toxin; erythematous hypersensitivity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ71612.
                                                                                                                                                                                                                                             nuclease; cystic fibrosis; vaccine;
s; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinuma Y, I
K, Takeda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                             pyogenes strain ATCC 14289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93JP-0037383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94EP-0101386.
                                                                                                                                            Location/Qualifiers
                                           /label= Mat_protein
                                                                                            /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; So
100.0%; P:
ative 0;
                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Igarashi H,
(, Yutsudo T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 203; DB 15;
Pred. No. 1.4e-22;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iwasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      group A streptococci; spe; ovrogenic exotoxin; blastogens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skin reaction; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z,
                                                                                                                                                                                                                                                                    immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kishishita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271;
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RRESULT 6
ABB93017
IID ABB93
XX AB93017
AC AB93
XX Stre
XX Telfe
Pi Telfe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                        27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                          Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes DNase B, including the leader peptide, has the amino acid sequence given in AAR8821. The enzyme can be obtd. on a large scale by expression of encoding DNA (AAT12774) in transformed host cells, esp. Escherichia coll. Inclusion in transformed host cells, esp. Escherichia coll. Inclusion of the leader peptide facilitates purification of the recombinant enzyme. The DNase B is useful in immunoassasys to detect anti-DNase B antibodies in serum as a marker for S. pyogenes infection, and is also useful as a vaccine or for treatment, via
                Telford J,
Tettelin H;
                                                           (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA encoding Streptococcus pyogenes DNase B - for recombinant prodn. of the enzyme in other bacteria, useful in immunoassays or for treating cystic fibrosis
                                                                                                                                                                     29-OCT-2001; 2001WO-GB04789.
                                                                                                                                                                                                   02-MAY-2002.
                                                                                                                                                                                                                                WO200234771-A2
                                                                                                                                                                                                                                                               Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                         Streptococcus polypeptide SEQ ID NO 9210.
                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP30017 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 67-70; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-151377/15.
N-PSDB; AAT12774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BECI ) BECKMAN INSTR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 delivery,
                                                           CHIRON SPA.
INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Belei MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 AA;
                                                                                                        ; 2000GB-0026333.
; 2000GB-0028727.
; 2001GB-0005640.
                            Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US09450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US09450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pang PPY
                            Margarit Ros
                                                                                                                                                                                                                                                                                                                                                                                                                                                      271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 203; DB 17;
Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                              YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17;
                              Grandi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                            Ó
                              Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
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RESULT 7
AAR70702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and contibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by the treatment or prevention of infection or disease caused by the treatment or prevention of infection or disease caused by the treatment or prevention of infection or disease caused by the treatment of particularly S. agalactiae and S. pyrogenes. Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Stroptococcus in a vaccine or diagnosting (I) or a nucleic acid encoding (I), may be used to detect streptococcus in a compound binds to cused as a vaccine or diagnostic composition. The disease caused by acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
            Adams
                                                                    23-JUN-1993;
                                                                                                  18-MAY-1994;
                                                                                                                                05-JAN-1995.
                                                                                                                                                           WO9500650-A1
                                                                                                                                                                                                    misc_difference
                                                                                                                                                                                                                                       Peptide
                                      (BECI ) BECKMAN INSTR INC.
                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                DNA-ase-B; diagnostic; vaccine; cystic fibrosis therapy
                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                        DNA-ase-B
                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR70702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR70702 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 4045; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-352536/38.
N-PSDB; ABN70648.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNLLGŚRRVFŚKKCRLVKFŚMVALVŚATMAVTTVTLENTALAR 43
            Belei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                          pyogenes (ATCC 14289)
                                                                 93US-0082845
                                                                                               94WO-US05626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                      274
         ã
                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                    /note= "mature protein<sup>|</sup>
1..45
                                                                                                                                                                                                           /note= "leader peptide: claim 11"
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
         Pang PPY;
                                                                                                                                                                                 "in-frame stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a protein (ABP25413-ABP30895) from group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 203; DB 23;
Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 8
AAU00294
ID AAU0
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                           20-OCT-1999;
20-JAN-2000;
07-SEP-2000;
                                        New interferon induced polypeptides and polynucleotides, useful for the diagnosis, prevention and treatment of immunological, cell proliferative disorders, such as lupus erythematosus, cancer, stroke and Alzheimer's disease
                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                            Interferon induced nucleic acid; autoimmune disease; lupus erythematosus; immunodeficiency; stroke; acquired immunodeficiency syndrome; AIDS; graft rejection; viral infection; hepatitis; aplastic anaemia; cancer; human immunodeficiency virus; HTV; immune-mediated glomerulonephritis; haematologic disease; chronic neutropenia; myocardial infarction; neurological disease; Alzhaimer's disease; Parkinson's disease; tumour; amyotrophic lateral sclerosis; spinal muscular atrophy; human; IFN2.
                                                                                                                      WPI; 2001-235201/24.
                                                                                                                                             Peyman JA, Da Silva A,
                                                                                                                                                                         (CURA-)
                                                                                                                                                                                                                                                 08-SEP-1999;
                                                                                                                                                                                                                                                                      08-SEP-2000; 2000WO-US24704
                                                                                                                                                                                                                                                                                                                       WO200118208-A2
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                 15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU00294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU00294 standard; Protein; 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the sequence shows a gene product corresponding pyogenes DNA-ase-B. The protein is useful as a vaccine or as an aerosol to trea excessive lung cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA encoding Streptococcus pyogenes DNase B - for diagnosing S. pyogenes infection, also new promoter for expressing other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 5; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence shows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995~052087/07.
N-PSDB; AAQ85037.
                                                                                                                                                                      CURAGEN CORP.
BIOGEN INC.
                                                                                                           AAS01147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 NILGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                        99US-0160575.
2000US-0177104.
2000US-0656633.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 AA;
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                                                                                                                                                                                                                                               99US-0152921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide,
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                                                                                                                                            Hochman
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Pred. No. 8.6e-22;
                                                                                                                                             ש
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFN2
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                                                                                                                                          Hsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to a Streptococcus diagnostic agent, viscosity, e.g. in
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The sequence

represents interferon induced polypeptide, IFN2.

IFN

Claim 1; Page 17-22; 134pp;

English

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RESULT 9
ABG52177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc pathology associated with IFN polypeptide in a human. They are useful for content of the presence of or predisposition to a disease associated cowith altered levels of IFN polypeptide or polynucleotide. IFN nucleic cc acids, polypeptides and antibodies are useful for diagnosis, prevention or treatment of variety of immunological and cell proliferative cc disorders, such as autoimmune diseases e.g. lupus erythematosus, cc immunodeficiency diseases such as acquired immunodeficiency syndrome cc (AIDS), graft rejection, viral infections including hepatitis and human claim immunodeficiency virus (HIV), immune-mediated glomerulomephritis, cc haematologic diseases such as aplastic anaemia and chronic neutropenia cc and cancer. In addition they are also useful for treating or diagnosing covarious disorders associated with cell death, including myocardial cc various disorders associated with cell death, including myocardial cc arrophy. IFN nucleic acids and polypeptides are also useful for clarophy. IFN nucleic acids and polypeptides are also useful for compounds which inhibit or enhance IFN activity or function and as targets for the identification of small molecules that care immunostimulatory, immunosuppressive, or stimulate or suppress normal could be a made to the identification of small molecules that are immunostimulatory, immunosuppressive, or stimulate or suppress normal could could be account of the process of the identification of small molecules that the identification of small molecules that are immunostimulatory, immunosuppressive, or stimulate or suppress normal including hypersuppressive, or stimulate or suppress normal could the process of the identification of small molecules that the identification of s
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26-MAY-2000;
30-JUN-2000;
                                                      Human genome-derived single exon nucleic acid probes analysing gene expression in human adult liver - \,
                                                                                                                           WPI; 2001-488898/53
                                                                                                                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human liver peptide, SEQ ID No 30825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2003
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                                                                                                                                                                                                              (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or tumour cell growth in mammals, including humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               903
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                                                                                                                                                                                                            MOLECULAR DYNAMICS INC
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|:| : |:| : | | | :|| ::: : | |::|
NILKGQNIFTKEAKL--FSFLALLNSYVPDTTISL 935
                                                                                                                                                                  Hanzel DK,
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                                                                                                                                                                                                                                                                     ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
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Pred. No.
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21;
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                                                                                 useful
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Claim 27;

SEQ ID No

30825; 658pp; English

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RESULT 10
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Best Local S
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. R8437348-R8G5930 represent human liver single exon encoded peptides of the invention.

Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
         The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derive from human breast and BT 474 cells. The expression involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA, of human breast, and then measuring the label
                                                                                                                                      New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                           Claim
                                                                                                                                                                                                                                       Penn SG,
                                                                                                                                                                                                                                                                                                                  21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-2002
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                                                                                                                                                                                                        WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #4764 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB32113;
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                                                                                                         27; SEQ
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                                                                                                                                                                                                                                    Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1591 AA;
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; 2000US-0207456.
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2000US-0234687.
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                                                                                                                                                                                                                                                                                                     2000GB-0024263
                                                                                                        ID NO 15081; 327pp + sequence listing; English
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; Pred. No. 21;
13; Mismatches
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RESULT 11
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              printed
from WIP
                                                              measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
                      Note: The sequence data for this patent did not form part printed specification, but was obtained in electronic form
                                                                                                                                                                                       The invention relates to a single exon nucleic acid
                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 30000; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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2000US-0608408.
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2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver; gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                               DK,
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                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
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Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                               Rank DR
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Query Match Best Local S Matches 12

Similarity

28.1%;

12;

Conservative

13;

Score 57; DB: Pred. No. 21; 13; Mismatches

22; 8

Length 1591;

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RESULT 12
ABB22654
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Best Local Similarity
Matches 12; Conserv
                             ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systemm e.g. cardiovascular disease. Appertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
 Sequence
                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                   measuring human
                                                                                                                                                            The present invention relates to single exon nucleic acid probes
                                                                                                                                                                                                                             Single
                                                                                                                                                                                         Claim 15;
                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                          exon nucleic acid probes for analyzing
                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS
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                                                                                                                                                                                     SEQ ID No 24424; 530pp; English.
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1591 AA;
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2000US-0236359
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2000US-0207456
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                                                                                                                                                 gene expression in a sample derived
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34.3%;
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Pred. No.
                                                                                                                                                                                                                                                                             Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for measuring heart
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21;
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RESULT 13
AAMS8054
ID AAMS8
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  RESULT 14
AAM70495
ID AAM70
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AC AAM70
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DT 06-N0
XX
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03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
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26-MAY-2000;
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Human bone marrow expressed probe encoded protein SEQ ID NO: 30801.
                                                       06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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04-OCT-2000;
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                                                                                                                                                     AAM70495 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epilepsy; cancer.
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2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                     Score 57; DB Pred. No. 21; 13; Mismatches
                                                                                                                                                        1591
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RESULT 15
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
04-FEB-2000; 2000US-0180312
26-MAY-2000; 2000US-0207456
30-JUN-2000; 2000US-0608408
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                                                                        09-AUG-2001
                                                                                                                                                                                                                                     AAM18331;
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                                               30-JAN-2001; 2001WO-US00670
                                                                                                WO200157278-A2
                                                                                                                        Homo sapiens.
                                                                                                                                                 cervical cancer.
                                                                                                                                                          Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                  Peptide #4765 encoded by probe for measuring cervical gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for
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27-SEP-2000;
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; 2000US-0234687.
; 2000US-0236359.
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2000US-0608408.
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Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human bone marrow
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Page 8
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Search completed: January 5, 2004, 18:38:05 Job time: 13.0866 secs
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Best Local Similarity
Matches 12; Conserv
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid probes (SENP: see AAI1068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID No 23157; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
                                                                    2 NLIGSRRVFSKKCRLVKFSMVALVSATMAVTTVTL 36
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905 NILKGQNIFTKEAKL--FSFLALLNSYVPDTTISL 937
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                                                                                                                                                                                                           1591 AA;
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; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
                                                                                                                                         Conservative
                                                                                                                                                         28.1%; Score 57; DB 22; 34.3%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
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                                                                                                                                         Mismatches
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                    Score
                 seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptcdatta/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdatta/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdatta/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdatta/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdatta/2/iaa/FCTUS_COMB.pep:*
6: /cgn2_6/ptcdatta/2/iaa/pcTUS_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd
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16, Appl
76, Appl
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44.5	45	45	45	45	45.5	45.5	45.5	45.5	45.5		46	46	46	46	46	48	48
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Sequence 1168, Ap	Sequence 26175, A	Sequence 17693, A	Sequence 1, Appli		<u>ب</u>	4.	4	Sequence 4, Appli		Sequence 4, Appli	Sequence 8, Appli	Sequence 4416, Ap	Seguence 22953, A	Sequence 4847, Ap	10	Sequence 17, Appl	Sequence 17, Appl

ALIGNMENTS

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US-08-393-889-1
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US-08-393-889-1
                                                                                                                      TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08393889
Patent No. 6420152
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 91001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/082,845
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                   MOLECULE TYPE: p
HYPOTHETICAL: NC
FRAGMENT TYPE: N
ORIGINAL SOURCE:
ORGANISM: Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Recombinant DNase B Derived from TITLE OF INVENTION: Streptococcus pyogenes NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Pasadena
STATE: Californ
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STREET: 2:
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                   Streptococcus pyogenes
                                                            N-terminal
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795-6321
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Query Match

100.0%; Score 203;

DB

4

Length 43;

Best Local Similarity

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; Sequence 8, Application US/08393889
Patent No. 6420152
; GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
                                                                                                    RESULT 3
US-08-393-889-8
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/APPLICATION NUMBER: US 08/APPLICATION DATE: 23-UIN-1993
ATTORNEY/AGENT INFORMATION:
NAME: May, William H.
REGISTRATION NUMBER: 26,76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (818) 795-6321 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Beckman Instruments, Inc.
APPLICANT: 2500 Harbor Boulevard
APPLICANT: Fullerton, California 92634
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: a
                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                     H: 43 amino acids
amino acid
OGY: linear
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2500 Harbor Boulevard
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                     Streptococcus pyogenes
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                          N-terminal
                                                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                              100.0%; Score 203; DB 5; 100.0%; Pred. No. 1.2e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                       APPLICANT: 2500 Harbor Boulevard
APPLICANT: Fullerton, California 92634
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Beckman Instruments,
APPLICANT: 2500 Harbor Boulevary
APPLICANT: Fullerton, California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 95:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
FILING DATE: 1
CLASSIFICATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                             ZIP: 92634
                                                                                                                                                                                                              STREET: 2500 Harbor Boulevard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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STREET: 771 forn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 100.0%;
Conservative
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225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (818) 795-6321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                            Beckman Instruments, Inc
                  18-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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Pred. No. 1.1e-22;
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                                                                                                                                                                                                                                                                                                                                                                      Inc.
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US-08-393-889-15
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PCT-US94-09450-8
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
                                                                                                              NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Adams, Craig W
APPLICANT: Pang, Patty P.
APPLICANT: Belei, Marina
                                                                   MOLECULE TYPE:
                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                  TOPOLOGY:
                                                                                                                                                                                                                             NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION: Recombinant DNase B Derived (TLE OF INVENTION: Streptococcus pyogenes DMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 26, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 91001
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                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California
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                                                                                                               272 amino acids
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225 South Lake Avenue, Ninth Floor
                                                                                                                                                                   (818)
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ilarity 100.0%;
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23-JUN-1993
                                                                                                                                                                795-6321
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Patty P.-Y.
 95.6%;
97.6%;
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RR: 39D-1357 PCT
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Score 194; DB 4;
Pred. No. 2.5e-21;
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Pred. No. 1.1e-22;
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                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         Query Match
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GENERAL INFORMATION:
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                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                             APPLICANT: KOYULI, DAVIG U
APPLICANT: Klapper, Davig U
APPLICANT: Rafnar, Thorunn
Mei-chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vc
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Beckman Instruments, Inc.
APPLICANT: 2500 Harbor Boulevard
APPLICANT: Fullerton, California 92634
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc
                                 NUMBER OF SEQUENCES:
                                               TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: May, William H.
REGISTRATION NUMBER: 26.
REFERENCE/DOCKET NUMBER:
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CLASSIFICATION:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                      76, Application US/08290448A
>. 5676954
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LAHIVE & COCKFIELD
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97.6%;
                                                                                                    David G.
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                                                                                                                                                                                                                                                                                                                                         Score 194; DB 5; Length 272; Pred. No. 2.5e-21;
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US-08-290-448A-76
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                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: USO8/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
EILING DATE: MUSUS 07/529,951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
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NAME: AMY E. MANDERSOURAS
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: IMI-018CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rogers, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
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CURRENT APPLICATION DATA:
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FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/529,951
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17 1000
                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02109-1875
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TTTY: Boston
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TOPOLOGY:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palan- "
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Pred. No. 2.
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   Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                               ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,069A
FILING DATE: December 29, 1993
PRIOR APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: MAYCH 17, 1989
APTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
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Best Local
                                                                                                                                                                     TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: IM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                 MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
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TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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LENGTH: 397 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                     TOPOLOGY:
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Local Similarity 36.8%;
hes 14; Conservative
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TELEPHONE: (617)227-5941
TELEPHONE: (617)227-5941
                                                                                                                                                         ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Amy E. Mandragouras
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NO. 577676
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                                                                                                                                                         397 amino acids
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                                                                                                 protein
                     27.3%;
Score 55.5; DB 1; Length 397; Pred. No. 2.4; 7; Mismatches 16; Indels
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Pred. No. 2.
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APPLICATION NUMBER: US 08/290,448
FILING DATE: 05-UWN-1995
APPLICATION NUMBER: US 07/529,951
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY AGENT INFORMATION:
NAME: Amy E. Mandragourae
NAME: Amy E. Mandragourae
INTORNEY AGENT NUMBER: 36,207
                                                                                                                                                                                                                                             Query Match 27.3%;
Best Local Similarity 36.8%;
Matches 14; Conservative
                                                        Sequence 76, Appli
Patent No. 6335020
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                                     GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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 APPLICANT:
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Method
TITLE OF INVENTION: Prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                      198 INVAGSSQIWIDHCSLSK-SFDGLVDVTLGSTHVTISN 234
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                                                                          Application US/08464000
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28 State Street
Rogers, Bruce
Klapper, Davi
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                                                                                                                                                                                                                                                                                                                                           protein
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; Pred. No. 2.4;
7; Mismatches
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                                                                                                                                                                                                                                                                                  Length 397;
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US-09-198-452A-472
US-09-198-452A-472
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                                                                                                                                                                                                                                                  Sequence 472, Application US/09198452A
PATENT NO. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preven
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 472
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APPLICATION UMBER: US/08/464,000
FILING DATE: 05-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 15-AUG-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
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INFORMATION FOR SEQ ID NO:
               FEATURE:
NAME/KEY: SITE
LOCATION: 1...927
OTHER INFORMATION: Xaa=unknown or other
                                                                                                     LENGTH: 927
TYPE: PRT
ORGANISM: Chlamydia
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LENGTH: 397 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: FC-DOS/MS-DOS
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NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,20
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TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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Local Similarity 36.8%;
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60 State Street
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DB 4; Length 927;

Query Match

Similarity

24.6%;

Score 50; DB Pred. No. 1.4; 9; Mismatches

2;

Length 50

Indels

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Best Local Similarity
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                                                            IELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amin
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                                                                                                                                               ATTUKNAL, ...

NAME: BENT, STEPHEN A
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1678
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                          MOLECULE TYPE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                              TOPOLOGY:
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SUITE 500, 1800 DIAGONAL ROAD
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WAGLAND, BARRY M
VENTION: VACCINE
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FRENKEL, MAURICE
GRANT, WARWICK N
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5; Mismatches
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Matches
                                                                                                             Sequence 64, Applicate Patent No. 6528702
GENERAL INFORMATION:
          APPLICANT: Salmeron, John
APPLICANT: Weislo, Laura
APPLICANT: Willits, Michael
APPLICANT: Willits, Michael
APPLICANT: Wengiste, Tesfaye
TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
FILE REFERENCE: S-30857A/RTPZ095
TURRENT APPLICATION NUMBER: US/09/519,232
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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Query Match
Best Local Similarity
Matches 11; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/07690983D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                            TELEFAX: (202)672-539
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: RUSSELL-JONES, Gregory J. APPLICANT: STEWART, Andrew G. APPLICANT: TSONIS, CON G. TITLE OF INVENTION: FUSION PROTEINS NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 24-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 25-JUN
                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 RLVKFSMVALVSATMAVITVTLENTALAR 43
                              15 RIVKFSMVALVSATMAVTTVTLENTALAR 43
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Pred. No. 9;
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Minimum DB :
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                              49.5
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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12 US-10-328-675A-64

11 US-09-847-208-13

12 US-10-287-274-300

15 US-10-129-851-5

10 US-08-983-5214

11 US-09-832-522-74
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1 US-09-847-208-15
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Sequence 1, Appli
Sequence 15, Appli
Sequence 15, Appl
Sequence 37952, A
Sequence 5042, Appl
Sequence 64, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 300, Appl
Sequence 300, Appl
Sequence 3069, Ap
Sequence 3069, Ap
Sequence 3069, Appl
Sequence 574, Appl
Sequence 74, Appl
Sequence 60, Appl
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Sequence 1193, Ap	933,	e 1027	e 1246	æ	e 4423	75	ς -	Sequence 6, Appli	e 8	e 122	Sequence 11177, A	Sequence 561, App	e 499	468,	738	e 61	5			Sequence 2191, Ap	80	e 40	e 72	e 1342	e 40,	e 12,	e 72,	Ø	Sequence 67, Appl

ALIGNMENTS

RESULT 1 US-09-119-900-1

; Sequence 1, Application US/09119900
Patent No. US2002008.622A1
; GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
; TITLE OF INVENTION: Recombinant DNas
; TITLE OF INVENTION: Streptococcus py FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796.4000 TELEPHONE: (818) 796-40 TELEFAX: (818) 795-6321 INFORMATION FOR SEQ ID NO: FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/082,845 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRIBATE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatil CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: CITY: Pasadena STATE: California ZIP: 91001 COUNTRY: ADDRESSEE: 225 South Lake Avenue, Ninth Floor USA Sheldon & Mak Recombinant DNase B Derived pyogenes Version

SEQUENCE CHARACTERISTICS:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09119900 Patent No. US20020081622A1
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
                                                                        Query Match
Best Local (
                                                            Matches
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                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Recombinant DNase B De
                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                        NAME: Farber, Michael B. REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sheldon & man
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
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                                                                        Similarity
                   MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
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MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
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Pred. No. 3.2e-21;
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Pred. No. 3.8e-22;
                                                          Mismatches
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                                                                                     Length 271;
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                                                         Indels
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US-09-119-900-15
                                                                                                                                                                                                                                                                                                                                                   US-09-864-761-37952
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Applicat: Patent No. US200200810 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         Sequence 37952, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                       FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                     APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Recombinant DNase B DeTITLE OF INVENTION: Streptococcus pyogenes NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NLIGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
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US20020081622A1
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                                                                                                                                                                                                                      Rank, David R.
Hanzel, David K.
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Belei, Marina
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97.6%;
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Pred. No. 6.5e-20;
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APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03 APPLICATION NUMBER: GB 24263.6

FILING DATE: 2000-10-04

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RESULT 5
US-09-847-208-15
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Sequence 15, Application US/09847208
Publication No. US20030082190A1
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 37952
                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
R OF SEQ ID NOS: 49117
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R INFORMATION:
R INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00664
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NILKGQNIFTKEAKL--FSFLALLNSYVPDTTISL
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EXPRESSED IN BRAIN, SIGNAL = 5.7
EXPRESSED IN BONE MARROW, SIGNAL = 4.6
EXPRESSED IN HEART, SIGNAL = 7.8
EXPRESSED IN HELA, SIGNAL = 5.8
EXPRESSED IN HELA, SIGNAL = 7.7
EST HUMAN HIT: BE888763.1, EVALUE 1.00e-113
SWISSPROT HIT: P50495, EVALUE 1.80e-02
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EXPRESSED
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IN ADULT LIVER, SIGNAL = 1.8
IN LUNG, SIGNAL = 3.5
IN PLACENTA, SIGNAL = 3.4
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NUMBER OF SEQ ID NOS: 177

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 397
TYPE: PRT
ORGANISM: Ambrosia artemisiifolia (Short ragweed)
US-09-847-208-15
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NUMBER PE
SOPTWARE: PE
; SEQ ID NO 12
TENCTH: 481
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                                                                                  PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1990-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
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SEQ ID NO 5042
LENGTH: 1019
                                                                                                                                                                                                                                                                                                                    Patent No. US2002005
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5042, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09767041 Patent No. US20020055168A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.3%; Score 55.5; Best Local Similarity 36.8%; Pred. No. 10; Matches 14; Conservative 7; Mismatches
                                                                                                                                                                                                                FILE REFERENCE: 2183-4726
CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/0
CURRENT FILING DATE: 2001-05-01
                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                          TITLE OF INVENTION: STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS FILE REFERENCE: 2183-4726
                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      575 RFFSRRCRHPCSGLSQKILLKFTFLSGARKVIISTNIAETSVTI 618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 RVFSKKCR------LVKFSMVA-----LVSATMAVTTVTL 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                               PatentIn version 3.0
                                                                                                                                                                                                                                                                                                   Smith, Hilda
                                                                                       MBER: EP98202467.1
1998-07-22
                                                                                                                                  1998-07-22
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Pred. No. 82;
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Query Match
Best Local Similarity
Thes 12; Conserve
                                                                         LENGTH: 396
; TYPE: PRT
; GRGANISM: Ambrosia artemisiifolia (Short ragweed)
US-09-847-208-13
                                                                                                                                                                                                                                                                                                                                                           US-09-847-208-13; Sequence 13, Application US/09847208; Publication No. US20030082190A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT ; ORGANISM: Beta vulgaris US-10-328-675A-64
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                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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SEQ ID NO 64
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Best Local :
                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
                                                                                                                                                                                                                                        TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES FILE REFERENCE: UC67.002A
                                                                                                                                                                                                                                                                                         APPLICANT: Saxon, Andrew APPLICANT: Zhang, Ke APPLICANT: Zhu, Daocheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 30857USNPDIV1
CURRENT APPLICATION NUMBER: US/10/328,675A
CURRENT FILING DATE: 2002-12-23
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APPLICANT: Weislo, Laura
APPLICANT: Willits, Michael
APPLICANT: Willits, Michael
TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/219,338
PRIOR FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 74
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ORGANISM: Streptococcus suis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENT 39
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Zhu, Daocheng
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                 Conservative
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            24.4%; Score 49.5; I
30.8%; Pred. No. 74;
tive 11; Mismatches
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Pred. No. le+02;
6; Mismatches
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Pred. No. 57;
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                                              DB 11;
                15;
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                                            Length 396;
                Indels
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                                                                                                                                                ; SEQ ID NO 5
, LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-129-851-5
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US-10-129-851-5
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                                                                                      Query Match
Best Local Similarity
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NUMBER OF SEQ ID NOS: 469
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 300
LENGTH: 728
                                                                          Matches.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10129851 Publication No. US20030120039A1
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Publication No. US20
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Xuan Mei Li
APPLICANT: Paul Robert Rosteck, Jr
APPLICANT: Eric Wen Su
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/129,851
                                                                                                                                                                                                                                                                                                                      APPLICANT: Jian-jun Wei
TITLE OF INVENTION: Human Preoptic Regulatory Factor-2 and Uses Thereof
FILE REFERENCE: X-12919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: ELITRA.008DV1
CURRENT APPLICATION NUMBER: US/10/287,274
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US-60/164415
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                 14 CRLVKFSMVALVSATMAVTTVTLENTAL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 ISISGSSQIWIDHCSLSK-SVDGLVDAKLGTTRLTVSNS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 RHIFSNKDFVIKFSTSVLQADKKEITIINKNENTTLTQ 97
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CYLIRFLQVFVQPANVAVTKMDVSNLAM 31
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5. US20030181408A1
                                                                          Conservative
                                                                                         24.1%;
                                                                                                                                                                                                                                                                                 2002-05-08
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                                                                                         Score 49;
Pred. No.
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                                                                        Mismatches
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                                                                                                           DB 15;
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                                                                                                           Length 75;
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                                                                      Indels
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RESULT 12 US-08-781-986A-5214

; Sequence 5214, Application US/08781986A

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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3069
LENGTH. 282
TYPE: PRT
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US-10-104-047-3069
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                                                                  ; ORGANISM: Homo sapiens
US-10-104-047-3069
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                                                                                                                                                                                                                                                                           Sequence 3069, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392
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Best Local
                              Query Match
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                Best Local Similarity
                                                                                                                                                                                                                            FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
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OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (301) 309-8504
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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24.1%; Score 49; DB
Local Similarity 33.3%; Pred. No. 35;
hes 11; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: 811
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 amino acids
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 Conservative
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                24.18;
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Score 49; DB
Pred. No. 59;
7; Mismatches
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                                DB 12; Length 282;
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 11;
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                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-832-522-74
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US-09-832-522-74
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                                                                Query Match
Best Local Similarity
Matches 11; Conserv
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LENGTH: 29
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CURRENT APPLICATION NUMBER: US/09/832,522
CURRENT FILING DATE: 2001-04-11
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PRIOR APPLICATION NUMBER: 60/220,644
PRIOR FILING DATE: 2000-07-25
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PRIOR APPLICATION NUMBER: 60/199,948
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PRIOR FILING DATE: 2000-04-11
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TITLE OF INVENTION: No. US20030091563A1el GPCR-Proteins and Nucleic Acids Encoding Sa
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81 SLMGNGYISLVQCILQVFFFIALASSEVAILTV 113
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Casman, Stacie J
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Szekeres, Edward S
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Padigaru, Muralidhara
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Pred. No. 63;
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RESULT 15
US-09-832-522-60
; Sequence 60, Application US/09832522
; Publication No. US20030091563A1
; GENERAL INFORMATION:

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Search completed: January 5, 2004, 19:13:43
Job time : 81.6648 secs
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CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/195,994
PRIOR FILING DATE: 2000-04-11
PRIOR PRIOR FILING DATE: 2000-04-11
PRIOR PPLICATION NUMBER: 60/196,538
PRIOR APPLICATION NUMBER: 60/220,644
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/264,851
PRIOR APPLICATION NUMBER: 60/264,851
PRIOR APPLICATION NUMBER: 60/299,964
PRIOR APPLICATION NUMBER: 60/199,964
PRIOR FILING DATE: 2000-04-27
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Best Local Similarity 33.3.
"***ches 11; Conservative
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SEQ ID NO 60
LENGTH: 303
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APPLICANT: Gangolli, Esha A
APPLICANT: Rastelli, Luca
APPLICANT: Smithson, Glennda
APPLICANT: Padigaru, Muralidhara
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PRIOR FILING DATE: 2000-04-27
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APPLICANT: Tchernev, Velizar T
APPLICANT: Szekeres, Edward S
APPLICANT: Grosse, William
APPLICANT: Alsobrook, John P
APPLICANT: Burgess, Catherine E
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A; Molecule type: protein A; Residues: 44-64 < IWW>

A;Accession: S36907 A;Molecule type: DNA A;Residues: 1-271 <IWA>

A;Cross-references: EMBL:D13428; NID:g432369; PIDN:BAA02693.1; PID:d1003198; PID:g432370 A;Accession: S36908

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T18158	T18868	C75015	T37628	E75202	S01757	D84474	S07997	B36119	S38001	C59434	C64127	E81077	B81865	H65208	T36317
hypothetical prote	myoblast city prot	probable pyrolysin	glycerol dehydroge	dipeptide abc tran	. lipoprotein traT p	hypothetical prote	lipoprotein traT p	preoptic area regu	probable serine/th	KIAA1688 protein (ADP-heptose syntha	fimbrial assembly	probable fimbrial	hypothetical 82.6	two-component sens

ALIGNMENTS

RESULT 1 S36907

C;Species: Streptococcus pyogenes
C;Date: 10-Dec-1993 #sequence revision 23-Feb-1996 #text_change
C;Accession: S35907; S36908; S29188
C;Accession: S36907; S36908; S29188
R;Iwasaki, M.; Igarashi, H.; Hinuma, Y.; Yutsudo, T.
FEBS Lett 331, 187-192, 1993

mitogenic factor, 25K, precursor - Streptococcus pyogenes

A; Title: Cloning, characterization and overexpression of A; Reference number: S36907; MUID:94009636; PMID:8405402

20

Streptococcus pyogenes gene

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15-Oct-1999

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A;Title: Evidence for lateral gene transfer between Archaea and A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: G72220 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-458 <ARN>
                                                                                                                                                                                                                      conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: G72220
C;Accession: G72220
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                       Nature 399, 323-329, 1999
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A;Title: A new type of mitogenic factor produced by Streptococcus pyogenes A;Reference number: S29188; MUID:92354761; PMID:1644200
A;Accession: S29188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;14-43/Domain: signal sequence #status predicted <SIG>
F:44-271/Product: mitogenic factor, 25K #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 44-64 < YUT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 100.0%; Score 203; DB 2 Similarity 100.0%; Pred. No. 7e-21; 43; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 271;
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chardson, D.;
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allergen Amb a I.3 - common ragweed C;Species: Ambrosia artemisiifolia (common ragweed) C;Date: 27-Nov-1991 #sequence_revision 03-Apr-1992 #text_change 29-Sep-1999 C;Accession: C39099 R;Rafnar, T.; Griffith, I.J.; Kuo, M.: Bood T. Biol. Chem 266
opine catabolism homolog yrbE - Bacillus subtilis C_\ellSpecies: Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 266, 1229-1236, 1991
A;Title: Cloning of Amb a I (antigen E), the major allergen family of short ragweed A;Reference number: A39099; MUID:91093235; PMID:1702434
A;Status: preliminary.
                                             D69972
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                                                          RESULT 5
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                                                                                                                                                                                                                                                                                                           A; Residues: 1-397 < RAF>
                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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A;Residues: 1-397 <GRI>
A;Cross-references: GB:M80560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: C53240
R;Griffith, I.J.; Pollock, J.; Klapper, D.C Int. Arch. Allergy Appl. Immunol. 96, 296.3 A;Title: Sequence polymorphism of Amb a I a A;Reference number: A53240; MUID:92234570; A;Accession: C53240 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergen Amb a I.3 precursor - common ragweed
C;Species: Ambrosia artemisiifolia (common ragweed)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 18-Sep-1998
C;Accession: C53240
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A;Experimental source: strain MSB8
                                                                                                                                                                                     Matches
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Best Local
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Best Local Similarity 44...
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                               Local Similarity 36.
les 14; Conservative
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                                                                                                                                                                                                                                                          pollen
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14; Conserv
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                                                                                                       INVAGSSQIWIDHCSLSK-SFDGLVDVTLGSTHVTISN 234
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                                                                                                                                                                                              27.3%;
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                                                                                                                                                                           Score 55.5; DI
Pred. No. 5.6;
7; Mismatches
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Pred. No. 5.
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Pred. No.
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a I and Amb a II,
4570; PMID:1809687
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     ftsE protein - Deinococcus radiodurans (strain R1)
c;Species: Deinococcus radiodurans
c;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: F75383
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F75383
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch: A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
                                                                                                                                                                                                                                                       A; Cross-references:
                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-366 < KLE>
                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: E69375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glodek, A.; Zhou, L.; Ove
Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y., M.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Scanlon, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A;Acthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Acthors: A;5580; MUID:38044033; PMID:3384377
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C;Superfamily: Streptomyces griseus strI protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not A; Molecule type: DNA
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C;Accession: D69972
C;Accession: D69972
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, N.M.; C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-341 <KUN>
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                                                                                                                                     Matches
                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Conserv
                                   RRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
RFVFTTKSRLIDFVAPAIIGVVTQMLAIILSSSSIAR
                                                                                                                           Conservative
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38.1%;
                                                                                                                  27.1%; Score 55; DB 2; Length 366; 29.7%; Pred. No. 6.1; tive 10; Mismatches 16; Indels
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M.; Cho
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J.A.;

Heidelberg,

J.F.;

Hickey, E.K.; Peterson,

J.D.; Dodson, R.J.; 1

Dupo

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A;Residues: 1-215 <ROE>
A;Cross-references: EMBL:Z49899; NID:g871513; PIDN:CAA90079.1; PID:g871514
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R;Roehl. T; Caliabe, A.; Seedorf, M.; Soll, J.
submitted to the EMBL Data Library, June 1995
                                                                                                                                                                                                                                                                                     GTP-binding protein - garden pea
N;Alternate names: small GTP-binding protein
C;Species: Pisum sativum (garden pea)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1019 <WUX>
A;Cross-references: EMBL:U97014; PIDN:AAB52427.1; GSPDB:GN00019; CESP:T05E8.
A;Experimental source: strain Bristol N2; clone T05E8
                                                                                                                                              A; Reference number: S57462
A; Accession: S57474
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A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                  A; Description: Pea mRNA for GTP-binding protein related
                                                                                                                                                                                                                                                                                                                                                    S57474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, April A;Description: The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Wu, X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T05E8.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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Superfamily: ras transforming protein; translation elongation 
f, Keywords: GTP binding; nucleotide binding; P-loop 
f, 16-131/Domain: translation elongation factor Tu homology <ETU-
;22-29/Region: nucleotide-binding motif A (P-loop)
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Best Local
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Pred. No. 9.5;
8; Mismatches
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Pred. No. 3
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cosmid T05E8
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B98287
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A;Sterror. B99287
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, are; P.W.
                                                                                                                                                                                                                                                                                                      R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrob
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                                                                                                                        A;Gene: AGR_L_2504
A;Map position: linear chromosome
                                                                                                                                                                                    A; Cross-references: GB: AE007870; PIDN: AAK89820.1;
                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-467 < KUR>
                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 22-Oct-2001 #sequence_revision
C;Accession: B98287
                                                                                                                                                                                                                                                                                                                                                                                                                                 probable transcription regulator [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: linear chromosome
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A;Experimental source: strain C58 (Dupont)
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F;159-161/Region:
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1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTAL
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                                                               Similarity
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Pred. No. 9.6;
8; Mismatches
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                                                           Score 52;
Pred. No.
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Pred. No. 18;
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                                                                                                                                                                                    PID:g15159752;
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Markelz, B.;
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Cer.

В.,

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RESULT 14
E86093
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
               A;Title: Genome sequence of enterohemorrhagic A;Reference number: A85480; MUID:21074935; PM:A;Accession: E86093
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein -
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A;Accession: S76798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystii
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Status:
                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA18710.1; Note: the nucleotide sequence was submitted to the EMBL Data Library, June
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura,
K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.;
A Res. 3, 109-136, 1996
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31.7%; Pred. No. 11
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PMID:11206551
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Yamada, M.; Ya
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Yamada, M.; Yasuda
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1996
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Search completed: January Job time : 10.989 secs

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2004, 18:42:46

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A;Residues: 1-728 <STO>
A;Cross-references: GB:AE005174; NID:g12518947; PIDN:AAG59209.1; GSPDB:GN00145; UWGP:Z56.
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: arp
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G91245
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                                                                                                                                                       A;Cross-references: GB:BA000007; PIDN:BAB38358.1; PID:g13364411; GSPDB:GN00154 A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                   DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G91245
                                                                                                                                                                                                                                                                                                  gasawara, N.;
                                                                                                                                                                                                                                                                                                                                regulator of acetyl CoA synthetase [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: G91245
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                                                                                                                           A;Gene:
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A; Residues: 1-728 <HAY>
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N.; Yasunaga, T.; Kuhara,
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1-22, 2001
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RHIFSNKDFVIKFSISVLQADKKEITIINKNENTTLTQ
                               RRVFSKKCRLVKFSMVALVSATMAVTTVTL-ENTALAR 43
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Pred. No. 37
                                                                           Score 51.5;
Pred. No. 37;
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Maximum Match 100%
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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    SwissProt_41:*
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    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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                                                                                         MURA HAEIN
MUA1 RHILO
YLJ1 CAEEL
LYS2 CANAL
                                                                                                                                                             NKX2 HUMAN
KG88 MOUSE
SRG3 CAEEL
YEBQ ECOLI
CYOB BUCAP
TRT1 SALTY
Y016 RICPR
                                                                                                                                                                                                                                                                    RFAE HAEIN
BIR3 MOUSE
KG88 HUMAN
KKR1 YEAST
KG88 RAT
TRT4 ECOLI
TOLQ_ECOLI
MENA_MYCLE
VF12_VACCC
FACF_HUMAN
LEU1_LACLA
GPMI_LEPIN
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MURA_RHIME
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7 rhizobium m
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	-	Q00126 ic		Q09344 ca	Q57389 ha	Q91q07 ar	028092 ar	Q9kka3 r		P14914 ri	054701 ra
caenorhabdi	clostridium	ictalurid h	ambrosia ar	caenorhabdi	haemophilus	arabidopsis	chaeoglob	outer mem	outer mem	rickettsia	ttus norv

ALIGNMENTS

RESULT 1

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EMBL; M62961; AAA32668.1; -.
EMBL; M80560; AAA32669.1; ALT_SEQ.
PIR; C39099; C39099.
InterPro; IPR002022; Amb_allergen.
Pfam; PF00544; pec_lyase; 1.
PRINTS; PR00807; AMBALLERGEN.
SMART; SM00856; Amb_all; 1.
SMART; SM00856; Amb_all; 1.
25 POTENTIAL.
STIGNAL 1 25 POLLEN ALLERGEN AMB A 1.3.
                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pollen allergen Amb a 1.3 precursor (Antigen E) (Antigen Amb a I).
Ambrosia artemisiifolia (Short ragweed).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eparmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Ambrosia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P27761;
01-AUG-1992
                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klapper D.G.; "Cloning of Amb a I (antigen E), the major allergen family of short
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ragweed pollen.";
J. Biol. Chem. 266:1229-1236(1991).
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RESULT 2
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RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Cappuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Entian K.D., Exrington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G.,
RA Ginesppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler B., Wedler H., Wattzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yata K.,
Pah Voshida K., Vashikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
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                                                                                                             Nature 390:249-256(1997)
                                                                                                                           "The complete subtilis.";
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Yoshida K., Yoshikawa
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M., Cutting S.M.;
encodes a putative
K checkpoint.";
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39,
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                                              PubMed=9025289;
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                                                                                                                                           Zumstein E., Yosh
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              regulator
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Gram-positive bacterium
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PIR; D69972; D69972.
Subtilist; BG12280; yrbE.
InterPro; IPR000683; GFO_IDH_MocA.
InterPro; IPR004104; GFO_IDH_MocA_C.
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Hypothetical protein yfcA.
YFCA OR B3327 OR C2873 OR Z3590 OR ECS
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Itoh T., Kimura S., Kitagawa M
Mizobuchi K., Mori H., Nakade (
Oshima T., Oyama S., Saito N.,
                                                                                                                                                                                                                                                      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli,
Escherichia coli 06, and
Escherichia coli 0157:H7.
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EMBL; Z99118; CAB14737.1; -.
EMBL; X93081; CAB43619.1; -.
PIR; D69972; D69972.
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                                                                                                                                                                                                                "The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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-!- SIMILARITY: BELONGS TO THE GFO/IDH/MOCA FAMILY.
                                                                      MEDLINE=97349980; Yamamoto Y., Aiba
                                                                                                                                       SEQUENCE
                                                                                                                                                                                       Science
                                                                                                                                                                                                                                     Mau B.,
                                                                                                                                                                                                                                                                                                                            MEDLINE=97426617; PubMed=9278503
                                                                                                                                                                                                                                                                                                                                                     STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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nce 277:1453-1474(1997).
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                     PubMed=9205837;
H., Baba T., Hayashi K., Inada T., Isono K.,
I., Kitagawa M., Makino K., Miki T., Mitsuhashi
i H., Nakade S., Nakamura Y., Nashimoto H.,
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Pred. No. 2;
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EMBL; AE005464; AAG57456.1; -.
EMBL; AP002561; BAB36634.1; -.
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                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Nhan C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Ye Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.,
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Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Mobley H.L. T., bonnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequen
of uropathogenic Escherichia coli.";
                                                                                                                                             PIR; C91030; C91030.
PIR; D85874; D85874.
PIR; S08346; S08346.
ECOGENE; EG11144; YfcA.
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or send an email to license@isb-sib.ch).
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Nature 409:529-533(2001).
[6]
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Yamagata S., Horiuchi T.;
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                                                                                               Pro; IPRO02781; DUF81.
PF01925; DUF81; 1.
herical protein; Transmembrane;
                                                                                                                                                                                                                                                    AE000321; AAC75387.1; D90863; BAA16183.1; -.
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Tobe T.,
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PRINTS; PR00149; FUMRATELYASE.
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HAMAP; MF_00006; -; 1.
InterPro; IPR003031; D_crystal
                                                                                                                                                                                                                                                                                                                         or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: Arginine biosynthesis; eighth (last) step
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=RHM002707;
MEDLINE=22337798;
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15-SEP-2003 (Rel.
15-SEP-2003 (Rel.
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NON TER 458 458
SEQUENCE 458 AA; 51030 MW;
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                                                                                                                                                                                                                                                                 InterPro; IPR000362; Fumarate_lyase.
                                                                                                                                                                                                                                                                                                                                     entities requires a
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                                                                                                                       NLLGSRRVFSKKC-RLV----KFSMVALVSATMAVTTVTLENTALAR
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Pred. No. 7.
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01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pollen allergen Amb a 1.1 precursor (Antigen E) (Antigen Amb Ambrosia artemisifolia (Short ragweed).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                                                                                                                 AMBAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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-!- FUNCTION: RESPONSIBLE FOR PREVENTING UNPRODUCTIVE CONJUGATION
BETWEEN BACTERIA CARRYING LIKE PLASMIDS.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Finlay B.B., Paranchych W.;
"Nucleotide sequence of the surface (from the IncFO lac plasmid pED208.";
J. Bacteriol. 166:713-721(1986).
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Ogata R.T., Winters C., Levine R.P.;
"Nuclectide sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
PLASMID=IncFII R100;
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MEDLINE=86223783; PubMed=3011738;
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Bacteria; Proteobacteria; Gammaproteobacteria;
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ITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Lipoprotein; Outer membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB Pred. No. 7.5; 9; Mismatches
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; A12C2AD8FACC437C CRC64;
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                          (Antigen Amb
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                                                                       Tracheophyta;
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ARPA_ECOLI
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STRAIN=K12 / MG1655,
MEDLINE=94089392; PubMed=8265357;
                                                                                             ARPA_ECOLI STANDARD; PRT; 728 AA P23325; P76781; Ol-NOV-1991 (Rel. 20, Created) Ol-OCT-1993 (Rel. 27, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat) Ankyrin-repeat protein A (Ankyrin-like regu ARPA OR ARP OR B4017.
                                                                                                                                                                                                                                                                                                                                                 CHAIN
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  Blattner F.R.,
                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A39099; A39099.
InterPro; IPR002022; Amb_allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M63116; -; NOT_ANNOTATED_CDS.
EMBL; M80558; AAA32665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Griffith I.J., Pollock J., Klapper D.G., Rogers B.L. "Sequence polymorphism of Amb a I and Amb a II, the in Ambrosia artemisiifolia (short ragweed) "; Int. Arch. Allergy Appl. Immunol. 96:296-304(1991).
                                                           NCBI_TaxID=562;
                                                                         Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of Amb a I (antigen B), the major allergen family of short ragweed pollen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rafnar T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4212
                                                                                                                                                                                                                                                                                                              POCGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: POLLEN AND FLOWERS.

PYM: The N-terminus is blocked.

DISEASE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.

SINILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.

AMB A I/AMB A II/CRY J I SUBFAMILY.
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                                                                                                                                                                                                                                                                                                 l Similarity
12; Conser
                                                                                                                                                                                                                                                  ISISGSSQIWIDHCSLSK-SVDGLVDAKLGTTRLTVSNS
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92
Burland V.D.,
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                                                                                   Gammaproteobacteria; Enterobacteriales;
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Pred. No. 1
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E -> D.
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regulatory
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Plunkett

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16-OCT-2001
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Olfactory re
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                                                        OSU1_HUMAN
Q9UGFS;
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"Analysis of the E
                                                                                                                                                                                                                                           CONFLICT
CONFLICT
                                                                                HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50088; ANK_REPEAT; FALSE_NEG.
PROSITE; PS50297; ANK_REP_REGION; FALSE_NEG.
Repeat; ANK_repeat; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumari S., Beatty C., Wolfe A.J.;
Unpublished observations (AUG-1996).
-!- FUNCTION: REGULATOR OF ACS SYNTHESIS.
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                           Repeat;
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Pfam; PF00023; ank; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuwald A.F., Green P.;
"Detecting patterns in protein sequences.";
J. Mol. Biol. 239:698-712(1994).
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Neuwald A.F., Gree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 97:149-150(1991).
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Cozzone A.J., Cortay J.-C.;
"Primary structure of the intergenic
the Escherichia coli chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 108-728 FROM N.A. MEDLINE=91138981; PubMed=1995
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MEDLINE=94285214; PubMed=8014990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 5 ANK repeats.
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                   (Rel. 40,
(Rel. 40,
(Rel. 40,
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to 92.8 minutes."
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                     Last sequence update)
Last annotation updat
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             (Hs6M1-28)
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Pred. No. 28;
7; Mismatches
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T -> S (IN REF. 1; AAC76987).
GFTDNPRYIABEKNYMEALLKKASEPHTVR
TLNLCLRRYA (IN REF. 2).
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Best Local
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28-FEB-2003
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                     transferase) (EPT).

MURA OR R00609 OR SMC02305.

Rhizoblum meliloti (Sinorhizoblum meliloti).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiahes;

Rhizoblaceae; Sinorhizoblum/Ensifer group; Sinorhizoblum.
                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC)
(Enoylpyruvate transferase) (UDP-N-acetylglucosamine
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CARBOHYD
SEQUENCE
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DOMAIN
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
                                                                                                                                                                   MURA
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Pfam; PF00001; 7tm_1; 1.
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Genew; HGNC:13971; OR5U1
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-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN
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                                                                                                                                                                   STANDARD;
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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BY SIMILARITY:
N-LINKED (GLCN)
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Pred. No. 14;
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                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                            Length 321;
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                                                                                                 (E)
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                     enolpyruvyl
                                                                                                   2.5
                                                                                                    .1.7)
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RFAE
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Best Local S
Matches 15
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Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Codrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
Tanalysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.",
Proc. Natl. Acad. Sci. U.S.A. 98.9877-9882 (201).
C. -- FUNCTION: Cell wall formation. Adds enolypruvyl to UDP-N-
acetylglucosamine (By similarity).
C. -- CATALYTIC ACTIVITY: Phosphoenolpyruvate + UDP-N-acetyl-D-
glucosamine = phosphate + UDP-N-acetyl-J-C-
Glucosamine = phosphate + UDP-N-acetyl-J-D-
Glucosamine = phosphate + UDP-N-acetyl-J-N-acetyl-J-D-
Glucosamine = phosphate + UDP-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-acetyl-J-N-ace
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HAMAP; MF_0011; --; 1.
IntearPro; IPR005750; AcGlu_Tran_MurA
InterPro; IPR001986; EPSP_Syntase.
Pfam; PF00275; EPSP_syntase; 1.
ProDom; PD001867; EPSP_syntase; 1.
TIGRFAMs; TIGR01072; marA; 1.
SEQUENCE FROM N.A.

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=9535030; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Wetdman J.F., Phillips C.A., Spriggs T., Saudek D.M., Brandon R.C.,

Weterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999
15-JUL-1999
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFAE HAEIN
005074;
                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
ADP-heptose synthase (EC 2.7.-.-).
RFAE OR WAME OR HI1526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAEIN
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                          Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Peptidoglycan synthesis; Cell wall; Cell division; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY: Peptidoglycan biosynthesis; first step.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the EPSP synthase family. MurA subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (S an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGARYVFPKVS--VGATHVLMMAATLANGTTVLGNAA 198
                                                                                                                                                                                                                                                                                                                                                 Proteobacteria; Gammaproteobacteria; Pasteurellales;
laceae; Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45434 MW; 48478C1A34167A25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.1%;
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Pred. No. 19;
7; Mismatches
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Best Local S
Matches 15
008863;
01-NOV-1997
01-NOV-1997
15-SEP-2003
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-Skeletal muscle;
MEDLINE-98110590; PubMed-9441758;
Liston P., Lefebvre C., Fong W.G.,
"Genomic Characterization of the r
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                                                                                                                                                                                                                                                                                    Genomics 46:495-503(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baculoviral IAP repeat-containing protein 1) (MIAP1) (MIAP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004821; Cyt tran rel.
InterPro; IPR004820; CytIdylyTtransf.
InterPro; IPR002173; pfkB.
InterPro; IPR002173; pfkB.
Pfam; PF01467; CTp transf_2; 1.
Pfam; PF00294; pfkB; 1.
TIGRPAMs; TIGR00125; cyt tran rel; 1.
PROSITE; PS00583; PFKB KINASES 1; FALSE NEG.
PROSITE; PS00583; PFKB KINASES 2; FALSE NEG.
Lipopolysaccharide bioSynthesis; Transferase; Complete SEQUENCE 476 AA; 51945 MW; 4F241C08D2C6951E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIRC3 OR BIRC2 OR IAP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; C64127; C64127
HSSP; P27623; 1COZ.
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PIR; C64127; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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Science 269:496~512(1995).
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-1- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES
                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing
                                                                                                                                                                             FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAFI FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECEUTITED MECROSIS FACTOR RECEPTOR 2 (THER2) (BY SIMILARITY).
                                                                                                                                                                                                                                                           FUNCTION: APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                          genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LADGRSFEESCYLANVAAGIVVGKLGTSTVSTVELENAIHAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGSRRVFSKKCRLVKFSMVALVS--ATMAVTTVTLENTALAR
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(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.1%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB
Pred. No. 21;
4; Mismatches
                                                                                                                                                                                                                                                                                                                       W.G., Xuan J.Y., Korneluk R.G., the mouse inhibitor of apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
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thi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1:
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                                                                                                                                                                                                                                 S REGION INTERACTS (TRAF1 AND TRAF2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43
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                                                                                                                                                                                                      TRAF2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration MBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
KG88_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
InterPro; IPR001841; Znf_ring.
Ifam; PF00653; BIR; 3.
Pfam; PF00619; CARD; 1.
Pfam; PF000619; zf-C3HC4; 1.
SMART; SM0023B; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00114; CARD; 1.
SMART; SM00114; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
ZN_FING
SEQUENCE
use by modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                            MEDLINE=21082932; PubMed=11214970;
Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XI:
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 7:347-355(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein KIAA1688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9COH5;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1197007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U88908;
HSSP; Q13490;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apoptosis;
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                       SIMILARITY: Contains 1 MyTH4 domain. SIMILARITY: Contains 1 Rho-GAP domain. SIMILARITY: Contains 2 WW domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.1%;
1 Similarity 31.6%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01282; BIR_REPEAT_1; 3.
PS50143; BIR_REPEAT_2; 3.
PS50209; CARD; 1.
non-profit
and this s
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PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 41,
(Rel. 41,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
167
253
436
553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birc2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67198 MW; AD7F73E6849317D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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is not
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIR 1.
BIR 2.
BIR 3.
CARD.
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RESULT 13
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         EMBL; 226878; CAA81516.1; -.
EMBL; 228171; CAA882013.1; -.
PIR; S38001; S38001.
SGD; S0001654; YKL171W.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002299; Sex_thr_pkinase
Pfam; PF00069; pkinase; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00784; MyTH4; 1.
Pfam; PF00620; RhoGAP; 1.
Pfam; PF00397; WW; 2.
SMART; SM00139; WYH44; 1.
SMART; SM00124; RhoGAP; 1.
SMART; SM00456; WW; 2.
                                                                                                                                                                                                          MEDLINE=94376719; PubMed=8091858; Vandenbol M., Bolle P.-A., Dion C., Portetelle D., Hilger F.; Vandenbol M., Bolle P.-A., Dion C., Portetelle D., Hilger F.; "Sequencing and analysis of a 20.5 kb DNA segment located on the arm of yeast chromosome XI."; Yeast 10:S25-S33(1994).

-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
KKR1 YE
P36003;
                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequenc
16-CCT-2001 (Rel. 40, Last annotat
Probable serine/threonine-protein
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB051475; BAB21779.1; ALT_INIT. HSSP; Q07960; 1RGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                    YKL171W OR YKL635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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IPR000198; RhoGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1083 AA;
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63
761
890
234
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                                                                                                                                                                                                                                                                                                                                                                                        58
97
879
1078
367
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WW_DOMAIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHOGAP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB 1
Pred. No. 49;
7; Mismatches
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WW 2.
MYTH4.
RHO-GAP.
PRO-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                782B213B1DCB4072 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1083;
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thr_pkinase

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KGBB_TAT 14
KGBB_TAT
ID KGBB
AC P1883
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Best Local S
Matches 14
                                                                                                           Query Match
Best Local (
                                                                                           Matches
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NP_BIND
BINDING
ACT_SITE
SEQUENCE
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P18890;
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PROSITE;
PROSITE;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein KIAA1688 homolog (Preoptic regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Transferase; Serine/threonine-protein kinase; ATP-binding.
                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcripts in the preoptic area and testis.";
Mol. Endocrinol. 4:1205-1210(1990).
-i- TISSUE SPECIFICTTY. n-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment, Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                         EMBL; X53232; CAA37324.1; ALT_FRAME. InterPro; IPR000198; RhoGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CAUTION: Was originally (Ref.1) thought to be a
secreted GNRH-like peptide.
-!- CAUTION: Ref.1 sequence differs from that shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Hypothalamus;
MEDLINE=91155954; PubMed=2293025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: Preoptic area and testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nowak F.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                      Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in positions 13 and 23.
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                                        14
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30
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PS00108;
PS50011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKIPFAERCRITIFISIQLISALKYMHSKTIVHGDIKLENCLIQK 590
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                                                                                                                                                                                                                                                 PS50238; RHOGAP;
                       CRLVKFSMVALVSATMAVTTVTLENTAL 41
CYLIRFLQVFVQPANVAITKMDVSNLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449
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928 AA;
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                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE ATP; 1.
PROTEIN KINASE ST; 1.
PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     912
463
478
580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence differs from that shown due to frameshifts
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                                                                                                           23.6%;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
POTENTIAL.
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Pred. No. 4
                                                                                                           Score 48; DB 1;
Pred. No. 5.9;
                                                                                                                                                                                                         RHO-GAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                 F216805966BE143E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P15177;
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There
                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RESPONSIBLE FOR PREVENTING UNPRODUCTIVE CONJUGATION BETWEEN BACTERIA CARRYING LIKE PLASMIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Escherichia.
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                                                                                                          SEQUENCE
                                                                                                                       LIPID
                                                                                                                                       CHAIN
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                                                                                                                                                              pROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Plasmid; Conjugation; Signal; Lipoprotein; Outer membrane.
                                                                                                                                                                                          EMBL; X14566; CAA32704.1; -. PIR; S07997; S07997.
                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               O'Connor D.;
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12;
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                         18 KFSMVALVSATMAVTTVTLENTALAR 43
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243 AA;
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                                                      Conservative
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25873 MW;
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                                                                                                            N-ACYL DIGLYCERIDE.
; B8305B10EFD81239 CRC64;
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Search completed: January 5, 2004, 18:39:08 Job time : 8.64272 secs

RESULT

Q81mi9 drosophila Q81mi9 drosophila Q41061 pisum sativ Q81028 agrobacteri Q85185 escherichia Q85820 gynechocyst P74602 synechocyst Q8405 escherichia Q8x405 escherichia Q9x405 escherichia Q9x06 escherichia Q9x06 escherichia Q9x08 arabidopsis Q9493 arabidopsis Q9403 arabidopsis Q94016 arabidopsis Q8pcf8 xanthomonas Q8pcf8 canthomonas Q8pcf8 callamydia t Q97g63 clostridium Q8xeq5 salmonella Q8d05 heliobacilla Q9adn1 streptomyce Q9adn1 streptomyce Q9adn1 streptomyce Q9adn1 streptomyce Q9adn1 gallid herp Q8f399 leptospira Q8f399 leptospira Q8f399 leptospira Q8eeb8 shewanella

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SEQUENCE FROM N.A.
STRAIN=SF370 / ATCC 700294 / Serotype M1;
STRAIN=SF370 / ATCC 700294 / Serotype M1;
STRAIN=SF370 / ATCC 700294 / Serotype M1;
SEDIM=21192649; PubMed=11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; Song L., White J., "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iwasaki M., Igarashi H., Hinuma Y., Yutsudo T.;
"Cloning, characterization and overexpression of a Streptococcus
pyogenes gene encoding a new type of mitogenic factor.";
FBBS Lett. 331:187-192(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2002 (TIENBLEEL. 22, Last annotation update)
Mitogenic factor precursor (Mitogenic factor, 25K).
MF OR SPY2043 OR SPYM18 2104.
Streptococcus pyogenes, serotype M18).
Bacteria, Firmicutes; Lactobacillales; Streptococcaeae;
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QBPTP4
QBPP57
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MEDLINE-94009636; PubMed-8405402;
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1 MNLLGSRRVFSKKCRLVKFS......LVSATMAVTTVTLENTALAR
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

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SEQUENCE Query Match

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Nagase T., Kikuno R., Ohara O.;
Submitted Sequence of a long cDNA clone isolated from human.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB059525; BAC23101.1; -.
Hypothetical protein.
NON TER 1
SEQUENCE 1595 AA; 184969 MW; 1DC92BE68887E662 CRC64;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Hypothetical protein; Compléte proteome.
SEQUENCE 458 AA; 49857 MW; 7C7E7D07F7DD4543 CRC64;
                                        1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein KIAA2004 (Fragment).
                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
11-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein TM1701.
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INTERPRO; IPR001014; Ribosomal_L23.
Pfam; PF01554; MATE; 2.
TIGREAMS; TIGR00797; MATE; 1.
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Best Local Similarity 44.4%
Matches 12; Conservative
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SEQUENCE FROM N.A.

C. STRAIN=MGAS8232 / Serctype M18;
X. MEDINE-21927393; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J.; Smoot L.M., Chaussee M.S.,
Smoot J.C., Barbian K.D., Wan Gompel J.J.; Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
A parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Rapur V., Daly J.A., Veasy L.G., Musser J.M.,
Genome sequence and comparative microarray analysis of serotype M18
IT Genome sequence strains associated with acute rheumatic fever outbreaks.";
Toutbreaks.";
Toutbreaks.";
Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
REMBL; D13428; BAB16053.1; -.
REMBL; AB006625; AAX34710.1; -.
REMBL; AB006625; AAX34710.1; -.
REMBL; AB010113; AAL98553.1; -.
REMBL; AB01011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.pyogenes; STRAIN=C203S; MEDLINE=21233096; PubMed=11335140; Gerlach D.; Schmidt K.H., Fleischer B.; Gerlach D.; Schmidt K.H., Fleischer B.; Haalc streptococcal superantigens (SPEX/SMEZ or SPEC) are responsible for the mitogenic activity of the so called mitogenic factor MF."; FEMS Immunol. Med. Microbiol. 39:209-216(2001).
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MEDLINE=22133808; PubMed=12122206;
MEDLINE=22133808; PubMed=12122206;
Mammarella N.D., Liu M.Y., Smoot J.C., Porcella S.F., Parkins L.D. Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlavevert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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271 AA; 30090 MW; 8FD8849E3CD01352 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Streptcodornase B precursor (Mitogenic factor 25K).
DNASEB OR MF OR SPYM3_1745.
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EMBL, AJ295272, CAC35734.1; -.
EMBL, AE014170, AAM80352.1; -.
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Best Local Similarity
Matches 43; Conserv
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Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Ketlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J. Lee N.H., Sutton G.G., Gill S., Kirkness E.R., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the hyperthermophilic, sulphate-teducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1991)
EMBL; AE001034; AAB90233.1; -.
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PRINTS; PR00164; ABC2TRNSPORT.
Hypothetical protein; ATP-binding; Complete proteome.
SEQUENCE 366 AA; 39790 MW; 46C9B836D02A9CBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea, Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) 25 transporter, ATP-binding protein, putative.
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                                                                                                          9 VFSKKCRLVKFSMVALVSATMAVTTVTLENTALA
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       Best Local Similarity 32.4%; Pred. No. 8.2;
Matches 11; Conservative 10; Mismatches
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MEDLINE=98049343; PubMed=9389475;
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Matches
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Amphibia, Batrachia, Anura, Archeobatrachia, Ascaphidae, Ascaphus
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Amphibia; Batrachia; Anura; Archeobatrachia; Ascaphidae; Ascaphus
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                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment).
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Last annotation update)
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                                                                                                                                                                              195 ILAPKLMLLNISMYLLLTSTWFLTMITLTTTKIS 228
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InterPro; IPR001750; Oxidored_q1.
Pfam: PF00361; oxidored_q1; 1.
NDJ: Oxidoreductase; Ubiquinone; Mitochondrion.
NON_TER
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InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
Nob; Oxidoreductae; Ub[quinone; Mitochondrion.
NON_TER 276 276
       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
                                                                                                                                       2 NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 6
Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 VFSKKCRLVKFSMVALVSATMAVTTVTLENTALA
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   28.1%; Score 57; DB 34.3%; Pred. No. 33; ive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ascaphus truei (tailed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16,
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                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Query Match
Best Local Similarity
Matches 12; Conserv
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Nielson M., Lohman K., Sullivan J.; "Phylogeography of the Tailed Frog (Ascaphus truei): Implications for the Biogeography of the Pacific Northwest."; Evolution 0:0-0(2001).
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"Brylogeography of the Tailed Frog (Ascaphus truei): Implications for
the Biogeography of the Pacific Northwest.";
Evolution 0:0-0(2001).
                                                                                     Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Ascaphidae; Ascaphus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion.
Skaryota Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Archeobatrachia, Ascaphidae, Ascaphus,
NCBI_TaxID=8439;
                                                                                                                                                                                                                                                                                                                                                                                                                                         // Match
Local Similarity 29.4%; Pred. No. 17;
Los 10; Conservative 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 26.1%; Score 53; DB 8; Length 271; Local Similarity 29.4%; Pred. No. 21; es 10; Conservative 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                209
22921 MW; F5A6039406541453 CRC64;
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            01-MAR-2003 (TrEMBLrel. 23, Last annotation update) NADH dehydrogenase subunit 2 (Fragment).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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(TrEMBLrel. 16, Last sequence update)
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InterPro; IPR001750; Oxidored q1.
Pfam; PF00361; oxidored q1; 1.
NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
                                                                                                                                                                                                                                                                               EMBL; AF277367; AAG36388.1; -.
InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
NAD; Oxidoreductase; Ubiquinone; Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 ILAPKLMVLNLSMYLLLTSTMFLTMITLTTTKIS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 VFSKKCRLVKFSMVALVSATMAVTTVTLENTALA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 VFSKKCRLVKFSMVALVSATMAVTTVTLENTALA 42
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                                                                    Ascaphus truei (tailed frog)
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209 AA;
                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                             NCBI_TaxID=8439;
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Q9G9E1;
01-MAR-2001 (
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NON TER
SEQUENCE
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EMBL; APONG170; BAC43997.1; -
Hypothetical protein; Complete proteome.

SEQUENCE 403 AA; 43742 MW; E65A78BA427BF54E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffar K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makazova K.S., Azavind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
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Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
NCBI_TaxID=28227;
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                                                                                                                   "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.6%; Score 54; DB 16; Length 403; 52.2%; Pred. No. 23; ive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.1%; Score 55; DB 16; Length 57
35.7%; Pred. No. 23;
tive 8; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                 576 AA; 63413 MW; 6167B2181D583DDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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(TrEMBLrel. 16, Last sequence update)
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                                                                                                                                                                                                            InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR00388; DUF214.
InterPro; IPR005286; IISP.
Pfam; PF00005; ABC tran; 1.
                                                                                                                                                                                                                                                                                                                                  ProDom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
TIGRFAMS; TIGR00960; 3a0501802; 1.
                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGR00960; 3a0501802; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 KFIKLFLASSTVALTTVTLSSCA 30
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                                                                                                                                                     Science 286:1571-1577(1999).
EMBL; AE001998; AAF11110.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 35.7
Matches 15, Conservative
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Best Local Similarity 52.2
Matches 12, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 576 AA:
                                                                                                                                       radiodurans R1.";
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01-MAR-2001 (
01-MAR-2001 (
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Archeobatrachia, Ascaphidae, Ascaphus
         01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01436; NADHDHGNASE2
                                                                                             Ascaphus truei (tailed frog)
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SEQUENCE 310 AA;
                                                                                                                                                                                                                NCBI_TaxID=8439;
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                                                                                                                                                                                                                                                                               Security Exception M., Lohman K., Sullivan J.;
Nielson M., Lohman K., Sullivan J.;
"Phylogeography of the Tailed Frog (Ascaphus truei): Implications for the Biogeography of the Pacific Northwest.";
Bvolution 0:0-0(2001).
EMBL; AF277364; AAG26385.1;
InterPro; IPRO1750, Oxidored_q1.
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Nielson M., Lohman K., Sullivan J.;
"Phylogeography of the Tailed Frog (Ascaphus truei): Implications i The Biogeography of the Pacific Northwest.";
Evolution 0:0-0(2001)
EMBL; AF277366; AAG26387.1; --
EMBL; AF277366; AAG26377.1; --
EMBL; AF277356; AAG26377.1; --
                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Archeobatrachia, Ascaphidae, Ascaphus,
NCBI_TaxID=8439;
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Amphibia, Batrachia, Anura, Archeobatrachia, Ascaphidae, Ascaphus,
NCBI_TaxID=8439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 AA; 30314 MW; B6F485CDF0068604 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last sequence update)
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NAD; Oxidoreductase; Ubīquinone; Mitochondrion.
NAD; Oxidoreductase; Ubīquinone; Mitochondrion.
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NAD; Oxidoreductase; Ubīquinone; Mitochondrion.
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                                                                                 Ascaphus truei (tailed frog)
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Best Local Similarity 29.4%
Matches 10; Conservative
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01-MAR-2001 (
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MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                           Gaps
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Phyllobacteriaceae; Mesorhizobium.
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                                                                                                             Query Match 26.1%; Score 53; DB 8; Length 276; Best Local Similarity 29.4%; Pred. No. 22; Matches 10; Conservative 11; Mismatches 13; Indels
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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NAD; Oxidoreductage; Ubiquinone; Mitochondrion.
NON TER 276 276
SEQÜENCE 276 AA; 30346 MW; 484F22D04EFSDFFE
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44.4%; Pred. No. 24;
tive 6; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                    310 AA.
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EMBL; AP003012; BAB54191.1; -.
InterPro; IPR00620; DUF6.
InterPro; IPR004626; RarD.
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TIGRFAMB; TIGR00688; rarD; 1.
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Search completed: January 5, 2004, 18:41:29 Job time: 16.9779 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

, Search time 3989 Seconds (without alignments) 11106.825 Million cell updates/sec nucleic search, using sw model 2004, 13:53:50 'n January . OM nucleic . С Run

US-08-482-785-7 Title: Perfect score:

1083 1 GACAACGCCTTCTTTTTCT......TGTGCAAAAAGCAAAAAGC 1083 Scoring table: Sequence:

2888711 segs, 20454813386 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

5777422 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

gb_ph: * * gb_ph: * * gb_ph: * * gb_pr: * gb_pr: * gb_nr: * gb_nr: * gb_ur: * gb_ur: * gb_ur: * gb_ur: * em_ba: * em_fur: * em gb_ba:* gb_htg:* gb_om:* em_hum:*

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Pred. No. is the number of results predicted by chance to have a em_htgo_mus:* em_htgo_other:*

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AJ295772 Streptoco ABO14158 Streptoco APO14158 Streptoco APO105143 Streptoco ARO19225 Sequence AE010084 Streptoco ARO19225 Sequence ARO19227 Sequence ARO19227 Sequence ARO19227 Sequence ARO1012 Streptoco AE014163 Streptoco AE014163 Streptoco ARO1012 Streptoco ARO10112 Streptoco ARO1012 Streptoco ARO10112 Streptoco ARO10112 Streptoco ARO10113 Sequence ARO10119 Arabidops ARO10119 Sequence ARO10119 Sequence ARO10119 Sequence ARO10119 Sequence AE014170 Streptoco AE005146 Streptoco AE006625 Streptoco D13428 Streptoco AE010113 Streptoco AE030578 Streptoco E08254 DNA encodin A49205 Sequence 11 AR21926 Sequence A49208 Sequence 14 AR219229 Sequence AR219229 SPY295272 AE014158 AP005143 A49204 AR219225 AE010084 SPSDAGENE AE010113 AB030578 E08254 A49205 AR219226 A49208 AE014170 AP005146 AE006625 STRMF AR219227 AF410852 AP005142 AE014163 I66494 AX344564 AY254474 AE010112 AB018119 AF269617 AX144937 ОВ 3334 29927 2942 2942 2942 2976 3350 6106 6106 7218 349980 Length Query 1042.8 1037.2 1030.8 961.6 922.6 922.6 853.8 Score 816 276.8 276.8 200 106.6 106.6 88.4 47.2 46.2 46.2 46.2 44.4 70. Result Š.

ALIGNMENTS 1083 bp Sequence 7 from Patent WO9606174. A49201.1 GI:2302733

RESULT A49201

PAT 07-MAR-1997

linear

Streptococcus pyogenes Streptococcus pyogenes Bacteria, Firmicutes; Lactobacillales; Streptococcaceae; DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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 781 ATTATGAAGTCGCTCCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGGTAT
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1 (Sassa I to 1083)
Adams, C.W., Pang, P.P.Y. and Belei, C.M.
Recombinant DNase B derived from Streptococcus patent: US 6420152-A 7 16-JUL-2002;
Location/Qualifiers
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; Pred. No. 1.1e-232;
0; Mismatches 0;
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AR219224
LOCUS
DEFINITION
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VERSION
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SOURCE
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Pred. No. 1.1e-232;
; Mismatches 0;
INSTRUMENTS INC (US)
Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 1083; Conservative 0;
BECKMAN
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/ products - C.a. peptidase predutedit
// protein_id="AAM80 33.1"
// db_xref="GI:21905476"
// translation="WRKKQKLPPIXLAILMSTSILLINAQSDIKANTVTEDTPATEQA"
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/ translation="WRKKQKLPPIXLAILMSTSILLINASPARATYGENERPIXLE
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/gene="emm3"
/note="best blastp hit: emb|CAA56449.1| (X80168) M3
protein [Streptococcus pyogenes]"
/cdon start=1
/transI_table=11
/product="antiphagocytic M protein, type 3"
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WARRLLQELNGEDVKKVLKNEIDOVTQLYTKHNSNYQQNAQAGRLDLRQKRGEKEYQDLKGDPDLAKQ
GYVLSDKHQQELBEKEKKYTRATAAVGGJSEELETVKQKVESTMQDLFKQNRVSQL
EQGLATTKQNAKEDPELAALANAADKQKLERAKIADETRLKEAKEDFELAALGHQHAH
NEYQAKLABKDDOJKGLESCKQILDASRKGTRRDLEAVRQAKATAEBLANNLKAELAK
VTEQKQILDASRKGTARDLEAVRQAKAQVEAALKQLEEQNRISEASRKGIRRDLDASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="best blastp hit: sp|P15926|SCA1_STRPY C5A peptidase
precursor (SCP)"
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EKDSSGQTPGKTPQKGQPSRTLEKRSSKRALATKASARDQLPTNDKDTNRLHLLKLV
MTTPFFGLVAHIFKTKRQKETKK"
                                                                                                                                                                                                                                                                             Direct Submission
Submitted (14-JUN-2002) Laboratory of Human-Bacterial Pathogenesis,
Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St.,
Hamilton, MT 59840, USA
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EDLPTTEYISPNEDGTFTLPEBAETMEGATVPLKMSDFTYVVEDMAGNITYTPVTNLL
      group A Streptococcus:
                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99 (15), 10078-10083 (2002)
2 (bases 1 to 53291)
Beres, S.B., Sylva, G.L., Barbian, K.D., Lei, B., Hoff, J.S.,
Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F.,
Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M. and
      Genome sequence of a serotype M3 strain of group A Streptococo
Phage-encoded toxins, the high-virulence phenotype, and clone

    53291
    organism="Streptococcus pyogenes MGAS315"

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/product="C5A peptidase precursor"
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/gene="scpA"
/note="synonym: SpyM3_1726"
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complement(4041. 5786)
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/strain="MGAS315"
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/transI table=
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1 (bases 1 to 53291)

Bersei,S.B., Sylva,G.L., Barbian,K.D., Lei,B., Hoff,J.S.,
Mammarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,
Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and
Musser,J.M.
                                                                                                                                 GCAAATTAGATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATG
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                                                                                                                                                                                                                      GCAAATTAGATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATG
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Streptococcus pyogenes MGAS315
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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AE014170 AE014074
AE014170.1 GI:21905475
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AGC 1083
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KEYWORDS
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AUTHORS
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EAKKQVEKOLANLTAELDKVKEEKQISDASROGLRRDLDASREAKKQVEKALEEANSK
LAALEKLINKELEESKKLTEKEKAELQAKLEAEAKALKEQLAKOAEELAKLRAGKASDS
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YAFFITWENSFLEVNOKUDKKYNNWHLINTXAFVAGVEKLMSSKENSISTNOLI
DLEEJEKQYDVITOVNWOGKSRLLLVIERSFNWONFLKKYIGEFFSITNFNBLDALTI
IKNPLDFHRKEVIFPTPPNKLHAPPSTS"
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KDKNDTKQPNSSDQSTPSPKDQSSQKESQNKDGRPTPBPDQQKDQTPDKTPERSADKT
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RHWTGDSAYTHNLLSRRYGITABQLDGFLNSLGIHYDKERLNGKRLLEWEKLTGLDVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complement (8788. 8519)
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/ gene="SpyM3_1730"
/ gene="SpyM3_1730"
/ note="best Diastp hit: gb|AAK34696.1| (AE006624)
/ hypothetical protein (mga-associated) [Streptococcus pyogenes MI GAS], and gb|AAL98548.1| (AE010111)
/ codon start=1
/ transl_table=11
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multi-gene activator"
/protein id="AAM80335.1"
/db_xref="G1:21905478"
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[Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="immunogenic secreted protein precursor"
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/db_xref="G1:21905481"
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/note="best blastp hit: gb|AAK34697.1|
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pyogenes MI GAS]"
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complement(5970, 7580)
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/note="synonym: SpyM3_1731"
complement(8597, .10225)
                                                                                                      complement (5970. .7580)
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                                                                            ATAGVAAVVKRKEEN"
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FSVTVGSITAXIVSRTSSRRILSMSQTAKKMVNLEPNLTCTIHGKDBIAMIASDINRL
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ETILLTQQQMKQLPQPPRPPRPDYSRNRKDGGTGLGLFTTHQILDQHHLAYRFVVLDQRWM
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BIPEHLKITSGTOFSEVPVGYKRSQPQNVLITYKSETYSFGQCTWYAYRKELGYQVD
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/gene="SpyM3_1732"
/gene="SpyM3_1732"
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/todon start=1
/trans1_table=11
AIVAIAMAESSLGTQGVAKEKGANMFGYGAFDFNPNNAKKYSDEVAIRHMVEDTIIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (1712. .12365)
/gene="SpyM3 1733"
/gene="SpyM3 1733"
/note="best blastp hit: gb|AAK34699.1| (AE006624) putative two-component response regulator [Streptococcus pyogenes M1 GAS], and gb|AAL98551.1| (AE010111) putative two-component response regulator [Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23280 ACAAGCATATGAATCTACTTGGATCAAGACGGGTTTTTTCTAAAAATGTCGGCTAGTAA 23221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TATTGATAAACTAGTTAAGTAAGCGTATACTATGGTTAGCTAAGCGAAATTAGAAAAGAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AATITICAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAAGAGTCACACTTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ATACTGCACTGGCACGACAAACACAGGTCTCAAATGATGTTGTTGTTCTAAATGATGGCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAA
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Pred. No. 1.3e-224;
); Mismatches 12; Indels 1; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
                                                                                             ESNVMGLGTISYRTFTAEQASLLTYVVGDKLPRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (11712. .12365)
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complement (11712. .12365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.7%; Sc. 98.8%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGAS8232] "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.8
Matches 1065; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRLYQVTHFNRKLLQKRLLLTLIETLLMGLVVFVANWLLGYAFKPTGRLTSLLYLLII
GGLGMTVYTALTLLTHQLDKLIGSKASRLRQKLGWH"
                      genome project
This clone was isolated from a patient presenting with toxic shock like syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative ATP-dependent protease proteolytic
                                                                                                                                                                                                                                                                        complement (422. .1012)
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identity 100 in 196 aa"
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3754. .5199
3764. .5199
/note="shiilar to GB:AAK33428.1 (AE006501) percent
identity 99 in 481 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2032. .3666)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="SPs1573"
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                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
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Fax:81-6-6879-2047)
                                                                                                                      source
                                                                                                                                                                                                                                          gene
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                                                                                             FEATURES
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                                                                                                  22860 CTGGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCG 22801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22620 ATTATGAAGTCGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGGTAT 22561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323825 bp DNA linear BCT 13-JUN-2003 Streptococcus pyogenes SSI-1 DNA, complete genome, section 6/6. AP005146 BA000034
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                                                                                                                                                                CTGGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTATGAAGTCGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGGTAT 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 841 CAATGCAATCTTCTGATAATACCATCAACGAGAAAGTATTAGTTTACAACACAGCTAATG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTACACCATTAACTACCATAACGGTACACCTACTCAAAAATAATACCAAAAGGCTAGAC 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021 TACTAGAAAAGCAATGATTGCCGTCATTGCTTTTTATGAATTTGTGCAAAAAGCAAA 1078
                                                                                                                                                                                                                                                            GAGATTTCTGGAATAGAAGTCATCTCATTGCAGATAGTCTCGGTGGAGATGCACTCAGAG
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Yamazaki,K., Okahashi,N., Kawabata,S., Yasunaga,T., Hattori,M.,
                                                                     TTGAAGGTAGCTACGGTGTTAGACAATCTTTCGGTAAAAATCAAAACCCCGCAGGATGGA
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TPESLDLFAMMABCYTNGMTHLIMEVSSQAYLVDRYYGLTFDVGVFLNISPDHIGPIE
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UDP-N-acetylmuramoylalanyl-D-glutamyl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon start=1 / experimental / transl table=11 / product="putative ferrichrome ABC transporter (permease) | product="putative ferrichrome ABC transporter (permease) | protein id="BAC64673.1" / db xref="G1:28811744" / translation="MCLERFCLKKTQIITKSHIFWLVFVLLSFSLCVAIYCHLRFGAV
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PGLLGINAGAGLALVIAYAFVPHIHYSLIILISLIGSSLAATIVFGLSYQSGKGYHQI
RLVLAGAMVSILLSALGQGITNYYHLANAVIGWQAGGLVGYNWQMIGYIAPLIILISLI
LAQLISYHLYTLSLGSSQARALGQKNNLISAVFMILVVLILSSAAVAIAGSISFIGLVI
PHLMKHFTPHHYRYLLDPLCAVSGASFWVWVDIACRNINPPYSTPLGALVSLIGFPGFL
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                  6-diaminopimelate ligase"
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/transl_table=11
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/db_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                GB:AAK33424.1 (AE006501) percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GB:AAL97173.1 (AE009984) percent identity 98 in 217 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 323825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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/product="conserved hypothetical protein"
/protein_id="BAC64675.1"
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Pred. No. 1.2e-224;
0; Mismatches 12;
                                                                                                                                  /evidence=not_experimental
/transl_table=11
/product="putative ferrichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (9270. .9923)
/gene="SP81580"
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                                /note="similar to GB:A
identity 98 in 345 aa"
'gene="SPs1579"
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                                                                                                     codon start=1
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Tue

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/gene="speak"// jobs// /gene="speak"// jobs// jobs/
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FYNETKNTELAQKAMLSLVISRVFETQYANKVSDKEVEKAYKQTADQYGTSFKTVLAQ

SGLPPETYKKQIRLYKLVEYAVKEQAKNETISKKDYRQAYDAYTPTMTABIMQFEKEE

DAKAALEAVKAEGADFAAIAKEKTTAADKKTYTFPSGETTLPAEVVRAASGLKEGNR

SEIITALDPATSKRTYHIIKNTKKATKKATKKAYOKKLKDIIVTGKLKDPDFQNKVIA

KALDKANVKIKDKAFANILAQFAKPNQKQPAQK"

COMPLEMENT (3134. . .3439)
                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAK34703.1"
/db_xref="G1:13623016"
/db_xref="G1:13623016"
/tb_xref="G1:100="WTGQKKLANLKKTDKKQ1IVRKTVDASVKLKVSKQKEHFIMKFK
KVUVIPALALAATCFLTACGTKKDSKKEEVKEIKMSDIKDDAVSKKTKVVDGEEVTEY
TTKDGNVIQIPAGNEEGMESKDAGGSGAPAKN"
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NFYSSDEWFRLANQPWDDIPCGVLSEDLLFDMIGDHNQLLADILDLAPIMYKHM"
/note="Best Blastp hit = pir||T27702 hypothetical protein
ZK1151.3 - Caenorhabditis elegans
>gi|3881532|emb|CAB07723.1| (Z93398) cDNA EST yk4e8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SPy2037"

/notes=Best Blastp hit = sp|p15294|PRTM_LACLA_PROTEASE
/notes=Best Blastp hit = spi|79978|pir||508083
probable protein export protein prtM precursor -
probable protein subsp. cremoris (strain NCD0 763)
plasmid plp763 - yei|47198|emb|CAA32349.1| (X14130) ORF (AA
1 to 299) [Lactococcus lactis subsp. cremoris]"
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complement (3134, .3439),
/gene="SPy2038"

/fene="SPy2038"

/note="the gene fragment has weak similarity to amino
acids 22-128 of pyrogenic exotoxin B; Best Blastp hit
gplAAAA5986.1| (L26157) pyrogenic exotoxin B

[Streptococcus pyogens9]"

complement (3441, .4637)
                                                                                                                   CDNA EST yk468.5 comes from this gene
CDNA EST EMBL:T00673 comes from this gene
CDNA EST yk20d2.5 comes from this gene
CDNA EST yk23g8.5 comes from this gene
CDNA EST yk37e2.5 comes from this gene
CDNA EST»
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/product="conversed hypothetical protein"
/protein_id="AAK34704.1"
/db_xref="GI:13623037"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (673. .969)
/gene="SPY2034"
/gene="SPY2034"
/note="Best Blastp hit = no blast hits"
/codon start=1
/transI_table=11
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/db_xref="G1:13623038"
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/note="synonym: SPy2039"
complement(3441, .4637)
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                                                                                                            from this gene
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/transT_table=11
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/trans1_table=11
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                                                                                                                                                                                                                                                                                GAGATTTCTGGAATAGAAGTCATCTCATTGCAGATAGTCTCGGTGGAGATGCACTCAGAG 188238
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                                                                                                                                                                                                                                                                                                                                                                              840
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1 (bases 1 to 12808)
Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Olan,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
Complete genome sequence of an MI strain of Streptococcus pyogenes Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
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Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S.,
Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J.,
Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
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Submitted (10-APR-2001) Department of Microbiology and Immunology,
University of Oklahoma Health Sciences Center, 940 SL Young Blvd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACTAGAAAAAGCAATGATTGCCGTCATTGCTTTTTATGAATTTGTGCAAAAAGCAAA 1078
                                                                                                 TCAATGCCGTTACAGGAACACGTACCCAAAATGTAGGAGGTCGTGACCAAAAAGGCGGCA
                                                                                                                                                                                                                                          TGCGCTATACCGAACAAAGAGCTCAAGAATGGTTAGAAGCAAATCGTGATGGCTATCTTT
                                                                                                                                                                                                                                                                                                                                                                       ATTATGAAGTCGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGGTAT
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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(mol_type="genomic DNA"
/strain="SF370"
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complement (242. .646)
gene="8Py2033"
complement (242. .646)
/gene="SPy2033"
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Streptococcus pyogenes M1 GAS
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                                                                                                                                                                                                                                                              Length 12808;
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                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                         Score 1044.4; DB 1;
Pred. No. 4.6e-224;
0; Mismatches 21;
   /gene="SPy2045'
                                                                                                                                                                                                                                                           96.4%;
98.1%;
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                      Similarity
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Best Local Simi
Matches 1057;
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                                          / Cranelation="MNKKKLGWRLLSTLALGGFVLANPVFADQNFARDEKEAKDSAIT
FIQKSAAIKAGARSAEDIKLDKVNLGGELSGSNMYYNISTGGFVIVSGDKRSPEILG
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SSNNPYFNHPRALEATSTRQYNWNNILPTYSGREGNVQKVAISELAMDVGISVDMDY
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FIEMVFSKVILNLDKKYRTKRYKGNESIRMFYNMLILFTQROBYDKASEILAKIEDYOL
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YEAAPIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Best Blastp hit = dbj|BAB16026.1| (AB030578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Best Blastp hit = emb|CAA59264.1| (X84793)
streptodornase [Streptococcus pyogenes]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative transcription regulator"
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/note="Best Blastp hit = no blast hits"
     Ē
/product="pyrogenic exotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [Streptococcus pyogenes]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: SPy2042"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="synonym: SPy2043"
complement(6661. .7476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (6661. .7476)
                                                                                                                                                                                            /gene="SPy2040"
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                                                                                                                                                                                                                                                                                                                                                                                                    5163. .5294
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                                                                                                                                                                                                                                                                                                                                                      "CLLADLAYQSA"
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986 GCAAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCCAACTATACAAAA 1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                        926 ATACTGCACTGGCACGACAAACACAGTCTCAAATGATGTTGTTCTAAATGATGGCGCAA 985
                                                                                                                                                                                                                                GACAATGCCTTCTTTTTTTTCCCTTATTATCTCGTTTAATTTTCATATTTTTAAAAAAAC
                                                                                                                                                                                                                                                   TATTGATAAACTTAGATAAAGCGTATACTATGGTTAGTGAGCGAAATTAGAAAAGAGG
                                                                                                                                                                                                                                                                                            ACAAGCATATGAATCTACTTGGATCAAGACGGGTTTTTTTCTAAAAAATGTCGGCTAGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAATGCCGTTACAGGAACACGTACCCAAAATGTAGGAGGTCGTGACCAAAAAGGCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1346 TCAATGCCGTTACAGGGACACGTACCCAAAATGTAGGAGGTCGTGACCAAAAAGGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCGCTATACCGAACAAAGAGCTCAAGAATGGTTAGAAGCAAATCGTGATGGCTATCTTT
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                                                                                                   Score 1042.8; DB 1; Length 2099;
Pred. No. 1.1e-223;
); Mismatches 22; Indels 0;
                                                                                                                                                                  GACAACGCCTTCTTTTTTCTCCTTACTATCTCCTTTAATTTTCATATTTT
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* 425 c 387 g 581 t
                                                                                                                               . . 0
                                                                                                   96.3%;
98.0%;
                                                                                                                  Best Local Similarity 98.0
Matches 1056, Conservative
        mat_peptide
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                                                                                                                                                                             CTCTGCTCACTAGGCCTAGCTTTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAAA 1020
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WARSHLIADSLGGALKVNAYTGRYGNVGSRDATINEKVLVYNTANGYTINYHNGTPTQK"
                                                                                                                                                                                                                                                                                                                                                       DNA linear BCT 19-JAN-2003 mitogenic factor, complete cds.
                                                    900
                                                                                                                   960
                                                                                                                                                                                                                                          TACTAGAAAAAGCAATGATTGCCGTCATTGCTTTTTATGAATTTTGTGCAAAAAGCAAA 1078
                                                                                                                                                                                                                                                            Streptococcae.

1 (bases 1 to 2099)

Iwasaki,M., Igarashi,H., Hinuma,Y. and Yutsudo,T.
Cloning, characterization and overexpression of a Streptococcus pyogenes gene encoding a new type of mitogenic factor FEBS Lett. 331 (1-2), 187-192 (1993)
                                                                CATGCATCTTCTGATAATACCATCAACGAGAAAGTATTAGTTTACAACACAGCTAATG
                                                                                                             GCTACACCATTAACTACCATAACGGTACACCTACTCAAAAATAATACCAAAAGGCTAGAC
CAATGCAATCTTCTGATAATACCATCAACGAGAAAGTATTAGTTTTACAACACCTAATG
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Submitted (24-Aug-1992) to DDBJ by:
Shionogi Institute for Medical Science
2-5-1 Mishima
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                       2099 bp
mf gene f
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81-6-6382-8336
tatanaka@ddbj.nig.ac.jp.
Location/Qualifiers
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D13428
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/gene="mf"
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/gene="mf"
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nuclease.
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Osaka 566
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/note="synonym: spyM18_2108"
complement(1877, .2965)
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complement(3703. 6120)
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Smoot, J.C., Barbian, K.D., Van Gompel, J.J., Smoot, L.M.,
Chaussee, M.S., Sylva, G.L., Sturdevant, D.B., Ricklefs, S.M.,
Porcella, S.F., Parkins, L.D., Beres, S.B., Campbell, D.S., Smith, T.M.,
Zhang, Q., Kapur, V., Dally, J.A., Veasy, L.G. and Musser, J.M.
Genome sequence and comparative microarray analysis of serotype M18
group, A. Streptococcus strains associated with acute rheumatic fever
CTCTGCTCACTAGGCCTAGCTTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAAA 1020
                                   AE010113
Streptococcus pyogenes strain MGAS8232, section 161 of 173 of the
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| Qaene="spyMis 2106"

| 1286. 1795

| / Gene="spyMis 2106"

| / note="best blastp match gb|AAK34711.1| (AE006625) protein

| low temperature requirement C [Streptococcus pyogenes Mi
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Smoot,J.C., Barbian,K.D., Van Gompel,J.J., Smoot,L.M.,
Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M.,
Dorcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,
Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.George. and Musser,J.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes MGAS8232
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (31-JAM-2002) Laboratory of Human Bacterial Pathogenesis/Rocky Mountain Laboratories/NIAID/NIH, 903 Hamilton, MT 59840, USA Location/Qualifiers
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complement (107. 922)
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complement (107. 922)
/gene="spyM18_2104"
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AE010113 AE009949
AE010113.1 GI:19749176
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/transl_table=1i
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putative pyruvate formate-lyase 2 [Streptococcus pyogenes
M1 GAS]" /gene="spyvil 2109" complement (3022 .3690) gene="spyvil 2109" /note="spyvil 2109" /note="best blastp match gb|AAK34713.1| (AE006625) putative transaldolase-like protein (Streptococcus /codon start=1 /transI_table=11 /product="putative transaldolase-like protein"
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gene

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gene

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180 240 300 360 480 540 931 871 811 691 420 631 009 9 991 751 571 511 451 720 331 780 271 840 211 391 GCAAATTAGATGAGTTAGGAAGGACGCGTACTAGAGGACGTACTAGAGGTACATTGACTTATGCCAATG GACAACGCCTTCTTTTTTCTCCTTATTATCTCGTTTAATTTTTCATATTTTTAAAAAAC AATITICAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAA ATACTGCACTGGCACGACAAACACAGGTCTCAAATGATGTTGTTCTAAATGATGGCGCAA ATACTGCACTGGCACACACACAGGTCTCAAATGATGTTGTTCTAAATGATGGCGCAA GCAAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAA CTTTAGGTACTAGTCAGATTACTCCAGCACTCTTTCCTAAAGCAGGAGATATTCTCTATA GCAAATTAGATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATG TTGAAGGTAGCTACGGTGTTAGACAATCTTTCGGTAAAAATCAAAAACCCCGCAGGATGGA CTGGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAAATGGTCTAATGTCG GAGATITCTGGAAIAGAAGTCATCTCATTGCAGATAGTCTCGGTGGAAGTGCACTTAGAG GCAAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAA GAGATTTCTGGAATAGAAGTCATCTCATTGCAGATAGTCTCGGTGGAGATGCACTCAGAG TCAATGCCGTTACAGGAACACGTACCCAAAATGTAGGAGGTCGTGACCAAAAAGGCGGCA ATTATGAAGCCGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGGTAT CTTTAGGTACTAGTCAGATTACTCCAGCACTCTTTCCTAAAGCAGGAGATATTCTCTATA TTGAAGGTAGCTACGGTGTTAGACAATCTTTCGGTAAAAATCAAAACCCCGCAGGATGGA CTGGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCG TGCGCTATACCGAACAAGAGCTCAAGAATGGTTAGAAGCAAATCGTGATGGCTATCTTT TGCGCTATACCGAACAAAGAGCTCAAGAATGGTTAGAAGCAAATCGTGTTATCTTTT **ATTATGAAGTCGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGGTAT** 1050 61 930 181 870 241 810 750 069 630 481 570 541 510 601 450 390 330 270 301 361 421 199 721 781 8 8 8 ద 요 유 ò ద 8 ద 8 ò В ⋧ ò ద 8 g ò g 8 g 8 셤 8

CAATGCAATCTTCTGATAATACCATCAACGAGAAAGTATTAGTTTTACAACACAGCTAATG 900 GCTACACCATTAACTACCATAACGGTACACCTACTCAAAAATAATACCAAAAAGGCTAGAC 960 210 CAATGCAATCTTCTGATAATACCATCAACGAGAAAGTATTAGTTTACAACACAGCTAATG 901 841 원 ò යු ò

CTCTGCTCACTAGGCCTAGCTTTTTACATCAAAAAAAGCAATGACTATAGAAAGTAAAAA CTCTGCTCACTAGGCCTAGCTTTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAAA 1050 TACTAGAAAAAGCAATGATTGCCGTCATTG 1 TACTAGAAAAGCAATGATTGCCGTCATTG 90 1021 961 ·8 8 ò

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                                                                                                                                            GACAACGCCTTCTTTTTCTCCTTACTATCTCCTTTAATTTTCATATT
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                                                                              Score 1030.8; DB 1;
Pred. No. 5.5e-221;
0; Mismatches 22;
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                                                                        Query Match
Best Local Similarity 97.9
Matches 1055; Conservative
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GKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGGAGGFNGYQGN
VGIKR!
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Submitted (29-JUL-1999) Kyongsu Hong, JCR Pharmaceuticals Co.,
Laboratories for Bicengineering and Research; 2-2-10 Murotani,
Nishi-Ku, Kobe 551-2241, Japan (E-mail:KOU@jcrpharm.co.jp,
Tel:81-78-991-4466, Fax:81-78-991-4465)
                                                                      AB030578.1 GI:10566901
exotoxin B; RopB; mitogenic factor.
Streptococcus pyogenes
streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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/Organism="Streptococcus pyogenes"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                               Unpublished
2 (bases 1 to 4334)
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303. .1118
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386

420 446 480 506 540 999 900 626 099 989 720 746 780 908

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PAT 07-MAR-1997
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267 ATACTGCACTGGCACGACAAACACAGGTCTCAAATGATGTTGTTCTAAATGATGGCGCAA
                                                                                                        327 CGAAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCCAACTATTACAAAA
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus
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Adams, C.W., Pang, P.P. and Belei, M.C.
RECOMBINATD DNASE B DERIVED FROM STREPTOCOCCUS
BECKMAN INSTRUMENTS INC (US)
LOCATION/Qualifiers
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Sequence 11 from Patent WO9606174.
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Takeda, Y., Igarashi, H. and Hinuma, Y.

Takeda, Y., Igarashi, H. and Hinuma, Y.

Takeda, Y., Igarashi, H. and Hinuma, Y.

MITOGENIC FACTOR, ITS GENE AND METHOD FOR DETECTING THE SAME GENE
SIENDOCOCCUE BYOGGENES

SI STEPLECOCCUE BYOGGENES

PR 32 STREPTOCOCCUE BYOGGENES

PR 04-OCT-1994

PR 04-OCT-1994

PR 01-FEB-1993 JP 93P

PR 01-FEB-1
CTCTGCTCACTAGGCCTAGCTTTTTACATCAAAAAAGCAATGACTATAGAAAGT-AAAA 1193
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                                          TACTAGAAAAAGCAATGATTGCCGTCATTGCTTTTTATGAATTTGTGCAAAAAGCAAA 1078
                                                              27 GACAATGCCTTCTTTTTTCTCCTTATTATCTCGTTTAATTTTTCATATTTTTTAAAAAAA 86
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Streptococcus pyogenes
Streptococcus pyogenes
Streptococcus pyogenes
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Streptococcus.
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/strain='NY-5'
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Pred. No. 2e-205;
0; Mismatches 14; Indels 1;
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/product='mitogenic factor'
Location/Qualifiers
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/organisme"Streptococcus pyogenes"
/mol_type="genomic DNA"
/db_xref="taxon:1314"
_195 c 199 g 278 t
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Matches 981; Conservative 0
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Adams.C.W., Pang,P.P.Y. and Belei,C.M.
Recombinant DNase B derived from Streptococcus pyogenes
Patent: US 6420152-A 11 16-JUL-2002;
Location/Qualifiers
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                                                                                                                                                               85.2%; Score 922.6; DB 6;
llarity 99.6%; Pred. No. 1.1e-196;
Conservative 0; Mismatches 4;
                        940 bp |
US 6420152.
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191 c 189 g
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Sequence 11 from p
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                                 Length 940;
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Pred. No. 1.1e-196;
0; Mismatches 4;
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/db_xref="taxon:1314"
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                            Query Match
Best Local Similarity 99.6%;
Matches 925; Conservative
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    TTAGGTACTAGTCAGATTACTCCAGCACTCTTTCCTAAAGCAGGAGATATTCTCTATAGC
                                                                       AAATTAGATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATGTT
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Adams, C.W., Pang, P.P.Y. and Belei, C.M.
Accombinant DNase B derived from Streptococcus
Patent: US 6420152-A 14 16-JUL-2002;
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Pred. No. 3.1e-181;
0; Mismatches 37;
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BECKMAN INSTRUMENTS INC (US)
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    note="unnamed protein product"

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/translation="MALLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQ
TOWNDVVLNDGASKYLNBALAWTFRDSPNYYKTLGTSQITPALFPKAGDILVSKLDE
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YEVAPIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK"
Gerlach,D., Schmidt,K.H. and Fleischer,B.
Basic Streptococcal superantigens (SPEX/SMEZ or SPEC) are
responsible for the mitogenic activity of the so-called mitogenic
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                                                                                                                                                               Direct Submission
Submitted (14-NOV-2000) Schmidt K.H., Institute of Medical
Microbiology, Friedrich-Schiller-University, Semmelweisstrasse
D-07740, GERMANY
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                                                                              30 (3), 209-216 (2001)
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                                                                                                                                                                                                                                                           1.816
/organism="Streptococcus pyogenes"
/mol_type="genomic DNA"
/strain="C2038"
1.816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.3%; Score 816; DB 1; Le
100.0%; Pred. No. 9.5e-173;
:ive 0; Mismatches 0;
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162 c 166 g 212
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/protein_id="CAC35734.1"
/db_xref="GI:13539553"
                                                                                                                                                                                                                                                                                                                                                                                                                               function="cleavage of
                                                                          FEMS Immunol. Med. Microbiol.
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complement (94. 1713)
/gene="deadD.1"
/fonce="synonym: SpyM3_1079"
/gene="deadD.1"
/gene="dead
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VRVKEQEKFDTMTRLMDVNQPELSIVFGRTKRRVDEITRGLKLRGFFABGIHGDLDQN
KRLRVIRDFKNDQIDILVATDVAARGLDISGYTHVYNYDITQDESYVHRIGRTGRAG
KSGSSITFVSPNEMGYLSMIENLTKKOMFDLRPATAEBAFQAKKVALKKIERDFADE
TIRSNFDKFKGDAVQLAAEFTPEELALYILGITVQDPDSLPFVBIARRKPLPFADE
GGGKGKGKGGKGGKTVARGGYRGDRNRDERDSDRRRQKRDGHDGSGNRDFK
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aqtgtgktaafglptlnkirtneniiqalviaptrelavqsqeelfregekgvkvrs
vyggssiekqikalksgahivvgtpgrlldlikrkalildhvetlildeademlnmgf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGFLHIRLASKVLQNWYYNLSWAINECLF"

complement (3812. .4507)
/gene="SpyW3 1082"

complement (3812. .4507)
/gene="SpyW3 1082"
/note="SpyW3 1082"
/note="best non-GAS blastp hit: gb|AAK75747.1 | (AE007460)
hypothetical protein [Streptococcus pneumoniae TIGR4]"
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3521...3742
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/noce="best blastp hit: gb|AAF61444.1|AF138858_1
(AF138858) polygalacturonase [Lycopersicon esculentum]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /producT="putative ATP-dependent RNA helicase"
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producE="conserved hypothetical protein"
protein id="AAM79689.1"
/db_xref="GI:21904820"
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/transl_table=
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Streptococcus pyogenes MGAS315, section 23 of 37 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus.

1 (bases 1 to 50081)
Beres, S.B., Sylva, G.L., Barbian, K.D., Lei, B., Hoff, J.S.,
Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F.,
Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M. and
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2 (bases 1 to 50081)
Bereo's.B., Sylva,G.L., Barbian,K.D., Lei,B., Hoff,J.S.,
Mammarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,
Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and
TGGAATAGAAGTCATCTCATTGCAGATAGTCTCGGTGGAGATGCACTCAGAGTCAATGCC
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Streptococcus pyogenes MGAS315
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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/organism="Streptococcus pyogenes phage 315.3"
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/errain="MGAS315"
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Location/Qualifiers
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AE014158.1 GI:21904816
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KEYWORDS
SOURCE
ORGANISM
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AE014158/c
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AUTHORS
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Page 18

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Gaps

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/note="best blastp hit: gb|AAK34235.1| (AE006579) putative formate dehydrogenase [Streptococcus pyogenes M1 GAS]" /codon start all fable=11
                                                                                                                                                                                                                                                                                                                                           /product="putative formate dehydrogenase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16659 TCGGTTAAATTTCAAAAATGTTAAAAAAGATTTGATTAACCAATTAAGTAAAACATATAA 16600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16502 TATCATCTCCTATATCATATCAACAGGCTACTTTAGC---TGATACTAAAGAAG 16446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16445 TTAATGTTGCTAATAGATATACTCCTCAGATACATATCTACCTGAAGCTTTGTCGTGGA 16386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 TATGGTTAGTTAGCGAAATTAGAAAAGAGGACAAGCATATGAATCTACTTGGATCAAGAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 CAAATGATGTTGTTCTAAATGATGGCGCAAGGAAGTACCTAAACGAAGCATTAGCTTGGA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 CAȚICAATGACAGTÇCTAACTAȚTACAAAACTTTAGGTACTAGȚCAGAȚTACTCCAGCAC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16599 TGTAATTAGTGAGAATAAAAAAAAAAAAAAAGAGGTCGAACAATGAAC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGTTTTTTCTAAAAAIGTCGGCTAGTAAATTTTTCAATGGTAGCTCTTGTATCAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 CAATGGCTGTAACAACAGTCACATTGAAAATACTGGAACTGGGACGACAAGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGCTAGAGGTACATTGACTTATGCCAATGTTGAAGGTAGCTACGGTGTTAGACAATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-----CGGTAAAATCAAAACCCCGCAGGATGGACTGGAAACCCTAATCATGTCAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 276.8; DB 1;
Pred. No. 8.4e-52;
0; Mismatches 362;
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COMPLEMENT (8719. 9498)
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58.9%;
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Matches 567
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                         FFLFLOLSQVIGLYTMYVLRGFPLDBALPLYHCRIAMLAIFFLPDRNKFKOLFMVLGI
GGTFLALLSPDLYPRLMHVANVSFYLGHYALLVNGILYLLBFYDASQLRLLSVVRXL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / LYAINGHEF 1013-MILTILESTAY TO AGAIN VSDLDDVPLHHIEFDSRKITKGDLFLD
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Result Š. 29-FEB-1996

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DNase B; nuclease; cystic fibrosis; vaccine; immunoassay; diagnosis; Escherichia coli; ds.
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AAD28382
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ABL70508
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 S. pyogenes DNaseB
Mitogenic factor g
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DNA-ase-B gene for
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S. pyogenes DNaseB
DNA-ase-B gene ups
                                                                                         January 5, 2004, 13:53:48 ; Search time 348 Seconds (without alignments) 8400.837 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                             US-08-482-785-7
1083
1 GACAACGCCTTCTTTTTCT......TGTGCAAAAAGCAAAAAGC 1083
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                      of hits satisfying chosen parameters:
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CTCTGCTCACTAGGCCTAGCTTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAA 1020
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                              TGCGCTATACCGAACAAAGAGCTCAAGAATGGTTAGAAGCAAATCGTGATGGCTATCTTT
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                                                                                                         recombinant
unoassays or
                                                                                                                                                                                                                                                                                                                                                         99.7%; Score 1079.8; DB 17; Length 1083; 99.8%; Pred. No. 2.9e-270; ive 0; Mismatches 2; Indels 0; (
                                                                                                            B - for recombina
l in immunoassays
                                                                                                                                                                                                                                                                                                                              Sequence 1083 BP; 377 A; 207 C; 205 G; 294 T; 0 other;
                                                                                                            DNase B
                                                                                                            New DNA encoding Streptococcus pyogenes prodn. of the enzyme in other bacteria, for treating cystic fibrosis
                                                                                                                                                                         Disclosure; Page 67-70; 115pp; English.
                                    PPY;
                                   Pang
      BECKMAN INSTR INC
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Matches 1081; Conservative
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P-PSDB; AAR88823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A modified DNase B gene (AAT12780) is the product of a PCR amplification of the Streptococcus pyogenes ATCC 14289 DNase B (AAT12774) from lambda clone 2-6. The modified gene codes for enzyme having an additional arguinne residue at the N-terminus (see AAR88825). The modified gene can be inserted into vector plasmid del-33 for prodn. of recombinant DNase B under control of the phage lambda pL promoter in Escherichia coli
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                                    AAQ71612 encodes a mitogenic factor which exhibits rabbit peripheral blood lymphocyte mitogenicity and/or DNA hydrolysing activity. It is strongly associated with group A Streptococci and the nucleotide sequences can be used for the microdetection of the gene and provide an early diagnosis of infectious disease caused by the bacteria. (See also AAQ71613-26)
                                                                                                                                                                                                    Gарв
                                                                                                                                                                       DB 15; Length 1021;
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                                                                                                                                                                                                    Indels
                                                                                                                                                other;
                                                                                                                                                                                                     16;
                                                                                                                                              Sequence 1021 BP; 349 A; 197 C; 197 G; 278 T; 0
                                                                                                                                                                                     .3e-239;
                                                                                                                     (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                       88.5%; Score 958.4;
98.3%; Pred. No. 9.3e
:ive 0; Mismatches
            Page 12-13; 20pp; English.
                                                                                                                                                                                                979; Conservative
                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA encoding Streptococcus pyogenes DNase B - for diagnosing
S. pyogenes infection, also new promoter for expressing other
proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence shows a construct used in fusion of a phage lambda promoter to DNA encoding a Streptococcus pyogenes DNA-ase-B. Binding sites for polymerase chain reaction DNA primers (given in AAQ85038 and AAQ85039) are shown. The product is useful in production of diagnostic agents, vaccines or therapy of cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.9%; Score 919.4; DB 16; Length 944; ilarity 99.4%; Pred. No. 1.2e-228; Conservative 0; Mismatches 6; Indels 0;
                                 DNA-ase-B; phage lambda promoter; diagnostic; vaccine; cystic fibrosis therapy; ds.
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           DNA-ase-B gene for fusion to phage lambda promoter.
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4.tag= a /product= DNA-ase-B
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                                                                     Streptococcus pyogenes (ATCC 14289)
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/codon= seq:AGA,
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complement
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                                      TTAGGTACTAGTCAGATTACTCCAGCACTCTTTCCTAAAGCAGGAGATATTCTTATAGC
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Streptococcus, GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds. Streptococcus polynucleotide SEQ ID NO 9209. ВР. ABN70648 standard; DNA; 813 (first entry) Streptococcus pyogenes 01-JUL-2002

40200234771-A2

02-MAY-2002

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenee), comparising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Wholeic acids encoding (I) are used to detect Streptococcus in a bening (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromogoraphy, immunoassays, and distinguishing/identifying 248 368 120 300 180 240 428 488 360 548 9 New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -ATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAAATACTGCA 129 ATGAATCTACTTGGATCAAGACGGGTTTTTTCTAAAAAATGTCGGCTAGTAAAATTTTCA ATGAATCTACTTGGATCAAGACGGGTTTTTTTTTTTTTAAAAAATGTCGGCTAGTAAAAATTTTCA 189 ATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAAATACTGCA CTAAACGAAGCATTAGCATTCAATGACAGTCCTAACTTTACAAAACTTTAGGT ACTAGTCAGATTACTCCAGCACTCTTTCCTAAAGCAGGAGATATTCTCTATAGCAAATTA ACTAGTCAGATCACTCCAGCACTCTTTCCTAAAGCAGGAGATATTCTCTATAGCAAATTA craaacgaagcarragcargacarrcaargacagrcccaacrarracaaaaccrraggr GATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATGTTGAAGGT GATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATGTTGAAGGT AGCTACGGTGTTAGACAATCTTTCGGTAAAAATCAAAACCCCGCAGGATGGACTGGAAAC Gaps ΰ ö 73.7%; Score 798.6; DB 24; Length 813; 98.9%; Pred. No. 2.6e-197; ive 0; Mismatches 9; Indels 0; Fraser ϋ Sequence 813 BP; 271 A; 165 C; 168 G; 209 T; 0 other; Grandi Masignani V, Margarit Ros YI, Claim 7; Page 4044-4045; 4525pp; English. 27-OCT-2000; 2000GB-0026333. 24-NOV-2000; 2000GB-0028727. 07-MAR-2001; 2001GB-0005640. Best Local Similarity 98.9 Matches 804; Conservative (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES Streptococcus proteins. WPI; 2002-352536/38. P-PSDB; ABP30017. 249 121 309 181 241 301 369 429 ò a ò 엄 ઠે 쉱 ò 요 8 g

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GTTACAGGAACACGTACCCAAAATGTAGGAGGTCGTGACCAAAAAGGCGGCATGCGCTAT 728

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ACCGAACAAGAGCTCAAGAATGGTTAGAAGCAAATCGTGATGGCTATCTTTATTATGAA 788
                           848
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                                                                           The sequence contains a cloned fragment encoding the N-terminal fragment of DNA-ase-B. The gene product is a marker of S. pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                New DNA encoding Streptococcus pyogenes DNase B - for diagnosing S. pyogenes infection, also new promoter for expressing other proteins
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129..400
/*tag= a
/product= DNA-ase-B N-terminal fragment
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                                                                                                                                                                                                                       DNA-ase-B2 N-terminal fragment clone; diagnostic;
                                                                                                       AAQ85036 standard; DNA; 400 BP
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(first entry)
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                                                                                                                                                                                                                                      Streptococcus pyogenes.
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P-PSDB; AAR70700.
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                                      36.9%; Score 400; DB 16; Length 400;
100.0%; Pred. No. 5.9e.94;
ative 0; Mismatches 0; Indels (
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                   DNase B; nuclease; cystic fibrosis; vaccine; immunoassay; diagnosis; Escherichia coli; ds.
                                                                                                                                                                                                                                                     Sequence 400 BP; 135 A; 77 C; 65 G; 123 T; 0 other;
infection. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                     S. pyogenes DNaseB DNA clone partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes strain ATCC 14289.
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
129.400
*tag= a
129.257
| tag= b
| 128.397
| *tag= c
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                                   Query Match 36.9%
Best Local Similarity 100.0°
Matches 400; Conservative
                                                                                                                                                                                                                                                                                                          AAT12773 standard; DNA; 400
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                                                                   1 GACAACGCCTTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 sig_peptide
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PCR; primer; ss
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                                                                                               23-JUN-1993;
                                       WO9500650-A1
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                                                         05-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                     Adams CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT12778;
   promoter
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                                                                                                                                                                                                                                                                                                                  AATTTTCAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAA 240
                                                                                                                                                                                                                                                                                                                                                                                 ATACTGCACTGCCACGACAAACACAGGTCTCAAATGATGTTGTTCTAAATGATGGCGCAA 300
                                                                                                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                                                      GCAAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAA 360
                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                   Lambda clone 2-6 (AAT12773) codes for Streptococcus pyogenes DNase B (AAR88821). It was obtd. from a library of S. pyogenes in vector lambda-gtil, established in Escherichia coli Y1090. The library was screened directly for enzymatic activity and postitive clone lambda 2-6 was recovered. The insert of this clone can be transferred to expression plasmids for large-scale recombinant DNase prodn. in E. coli. Fragments of the DNA can also be used as probes or primers.
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Promoter; DNA-ase-B gene upstream region; transcription start site; -10 region; -35 region; gene cloning; ds.
                           New DNA encoding Streptococcus pyogenes DNase B - for recombinant prodn. of the enzyme in other bacteria, useful in immunoassays or for treating cystic fibrosis
                                                                                                                                                                                                       ö
                                                                                                                                                                                  Query Match

36.9%; Score 400; DB 17; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.9e-94;
Matches 400; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTAGGTACTAGTCAGATTACTCCAGCACTCTTTCCTAA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTTAGGTACTAGTCAGATTACTCCAGCACTCTTTCCTAA 400
                                                                                                                                                                Sequence 400 BP; 135 A; 77 C; 65 G; 123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-ase-B gene upstream region and promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pyogenes (ATCC 14289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                 Claim 3; Fig 3; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ85040 standard; DNA; 200
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(first entry)
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/*tag=
61..69
/*tag=
WPI; 1996-151377/15.
          P-PSDB; AAR88821
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15-AUG-1995
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-10_signal
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121 ACAAGCATATGAATCTACTTGGATCAAGACGGGTTTTTTCTAAAAAATGTCGGCTAGTAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ACAAGCATATGAATCTACTTGGATCAAGACGGGTTTTTTTCTAAAAAATGTCGGCTAGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence upstream of a Streptococcus pyogenes DNA-ase-B gene open reading frame is shown. Transcription data suggest that there are 2 possible start sites, positions 96 and 97, for RNA-polymerase. The region contains a promoter, and -10 and -35 regions are shown. The promoter may be used to express S. pyogenes proteins in other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA encoding Streptococcus pyogenes DNase B - for diagnosing S. pyogenes infection, also new promoter for expressing other proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 200 BP; 66 A; 30 C; 31 G; 73 T; 0 other;
96..97
/*tag= c
/note= "Alternative start sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
18.5%; Score 200; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-42;
Matches 200; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prokaryotic cells. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 AATTTTCAATGGTAGCTCTT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Fig 7; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Pang PPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 AATTTTCAATGGTAGCTCTT
                                                                                                                                                                                                                                                                                     93US-0082845.
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                                                                                                                                                                                                                                                                                                                                          (BECI ) BECKMAN INSTR INC.
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                                                                                                                                                                                                                                                                                                                                                                                                     Belei CM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            610 AAGAATCCTGATGTTTATGTATTCTACAGTGCCATCCCTGAATATCAGGGGGCTGAGTTA 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              819 ATTCCAAGAGCTGTCGTGGTATCAATGCAATCTTCTGATAATACCATCAACGAGAAAGTA 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              670 Traccaacatcacirrraciatraccrrrarcriccaarcacraatraarcaaacreir 729
                                                                                                                                                                                                     The invention relates to a recombinant streptodornase and a process for its mass production from mutated Streptococcus equisimilis. This polynucleotide sequence represents a 966nt DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTGGAGGAAAGTCCATACGGAAAATGCTATTACTGGAACTCAAATGCAAAATGTGGGG
                                                                                                                                                                                                                                                                                                                                                                          579 TTAAATGGTCTATCTTATGTCGGAGATTTCTGGAATAGAAGTCATCTCATTGCAGATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                          639 CTCGGTGGAGATGCACTCAGAGTCAATGCCGTTACAGAACACGTACCCAAAATGTAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              759 GCAAATCGTGATGGCTATCTTTATGAAGTCGCTCCAATCTACAACGCAGACGAGTTG
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                            process for its mass production from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              879 TTAGTITTACAACACAGCTAATGGCTACACCATTAACTACCATAACGGTACAC 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     730 CGIGITITCAACACCGCTGAIGGATITAAIATAATIATGAAAAGGGGGGC 781
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                                                                                                                                                                                                                                                                                                      Ouery Match

8.2%; Score 88.4; DB 21; Length 966;
Best Local Similarity 55.4%; Pred. No. 6.1e-13;
Matches 195; Conservative 0; Mismatches 151; Indels 6
                                                                                                                                                                                                                                                                      Sequence 966 BP; 363 A; 157 C; 184 G; 262 T; 0 other;
                                                            Sohn HJ
                                                                                                                       Recombinant streptodornase and promutated Streptococcus equisimilis
                                                                                                                                                                     Disclosure; Page 3; 11pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
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                                                                                                                   Recombinant streptodornase
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97US-064964P.
                                                         Lee HH,
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                                                                                       WPI; 2000-408398/35
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                     (LEEH/) LEE H H.
                                                       Kim IC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6380370-B1
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08-NOV-1997;
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                                                     Bae S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAATACTGCACTGGCACGACAAACACAGTCTCAAATGATGTTGTTGTAAATGATGGCG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 TAAAATTTTCAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Addonatiganiccanacigoriocorocorometriroromanana incororiog
                                                                                                                                                                                                  New DNA encoding Streptococcus pyogenes DNase B - for recombinant prodm. of the enzyme in other bacteria, useful in immunoassays or for treating cystic fibrosis
                                                                                                                                                                                                                                                                                               A PCR primer pair (AAT12778-79) was used for the amplification of Streptococcus pyogenes ATCC 14289 DNase B gene (see AAT12774).
Use of these primers gives a product that is processed identically to native DNase B when inserted into vector plasmid del-33 and expressed in Escherichia coli transformants. The N-terminal sequence of the recombinant DNase B is identical to that of the native mature enzyme (AAR88824). Highly purified DNase B can be obtd. in large quantities.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17; Length 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 182 BP; 40 A; 49 C; 42 G; 51 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.8%; Score 106.6; DB 1.
77.3%; Pred. No. 6.5e-18;
ative 0; Mismatches 39
                                                                                                                                                                                                                                                                    Example 12; Page 54; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             966nt DNA sequence of the invention.
                                                                                                                                         Pang PPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK99137 standard; DNA; 966 BP.
                                     94WO-US09450.
                                                                   94WO-US09450.
                                                                                                  (BECI ) BECKMAN INSTR INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 77.3
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                   Belei MC,
                                                                                                                                                                    WPI; 1996-151377/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGC 182
                                18-AUG-1994;
                                                                 18-AUG-1994;
29-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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                                                                                                       ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABPS1244 to ABB27960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to soreen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP;
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                                               Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                             Gaps
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cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism;
cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour suppressor gene derived chemically modified sequence #151
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                                                                                                                                                                                                                                                                                  Score 47.2; DB 24; Length 2409;
Pred. No. 0.042;
0; Mismatches 158; Indels 0;
                                                                                                                                                                                                                                                           Sequence 2409 BP; 857 A; 314 C; 523 G; 715 T; 0 other;
                                                                                   Disclosure, SEQ ID 904; 267pp; English.
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Best Local Similarity 47.3%;
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           WPI; 2002-381255/41
                         P-PSDB; ABP38896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (58) and sequences complementary to (58). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for nallysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and old therapy of existing diseases or the predisposition to specific diseases by analysing controling methylations.
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                                                                                                                                                                                                                                                                                                                                                    Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITICIAAAAAAIGICGGCIAGIAAAAITITICAAIGGIAGCICITGIAICAGCCACAAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 GCTGTAACAACAGTCACACTTGAAAATACTGCACTGGCACGACAAAACACAGGTCTCAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6106 BP; 1938 A; 30 C; 849 G; 3289 T; 0 other;
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18.3%; Pred. No. 0.11;
ive 0; Mismatches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 151; 27pp; English
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                                                                                                                                                                                                Berlin K;
30-JUN-2000; 2000DE-1032529. 01-SEP-2000; 2000DE-1043826.
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Matches 158; Conservative
                                                                                                                                                                                                Piepenbrock C,
                                                                                                                       ÄĞ.
                                                                                                                       (EPIG-) EPIGENOMICS
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Page 10

us-08-482-785-7.rng

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Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDHG; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                          New nucleic acid, oligonuclectides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer
                                                Human chemically pretreated gene sequence #57 strand 1.
                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 113; 24pp; English.
                                                                                                                                                                                                              Berlin K;
    ВР
ABK40031 standard; DNA; 6106
                                                                                                                                                  29-JUN-2001; 2001WO-EP07470.
                                                                                                                                                                 30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                  (first entry)
                                                                                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                           WPI; 2002-154757/20.
                                                                                                                  WO200202806-A2.
                                                                                                   Homo sapiens,
                                 21-MAY-2002
                                                                                                                                   10-JAN-2002
                                                                                                                                                                                                          Olek A,
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The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of green sassociated with pharmacogenomics according to one of the sequences of the genes ALDHE (NW 00693), CYPILA (NW 00781), CYPILBI (NW 00497), CYPRA3 (NW 00679), COLN (NW 00279), COLN (NW 00597), COLN (NW 00597), UGT8 (NW 001010), EPHX2 (NW 004996), NM 019900, NM 019901, NM 01380), UGT8 (NW 004396, NM 019900, NM 019902, NM 019862, NM 019869, CC (NW 004996, NM 019900, NM 019901, NM 019869, NM 019899, NM 019890, NM 019890, NM 019890, NM 019800, NM 019890, NM 019809, NM 019800, NM 019809, NM 019800, NM 019809, NM 019809, NM 019809, NM 019809, NM 019800, NM 018800, NM 0188 Sequence 6106 BP; 1938 A; 30 C; 849 G; 3289 T; 0 other; ftp.wipo.int/pub/published_pct_sequences.

Best Local Similarity 48.3%; Score 46.2; DB 24; Length 6106; Matches 158; Conservative 0; Minmac. 0.11;

Gaps 1,

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5289 AAAATTAACTAAAAAATACGACAAAAAATCTTATTTTTCTCCCCCTATTTACACTAATT 5230 5229 fifitifactakaarakakakakakakitcitakitcikaritakaritakatrakakak 216 GCTGTAACAACAGTCACACTTGAAAATACTGGCACTGGCACAAAAAAAGAGGTCTCAAAT 275 276 GAIGITGITCIPAAATGATGGCGCAAGCAAGTACCIAAACGAAGCATTAGCTTGGACATTC 335 156 TITICIAAAAATGTCGGCTAGTAAATTTTCAATGGTAGCTCTTGTATCAGCCACAATG 5050 AAAATAATCTCTAAATCTTTAAAATCT 5024 336 AATGACAGTCCTAACTATTACAAACT 362 ò g g 8 d à ò 셤

ABL33472 standard; DNA; 6106 (first entry) 26-MAR-2002 ABL33472; RESULT 14 ABL33472,

Human immune system associated gene SEQ ID NO: 1445.

Human, immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthrift; antidiabetic; antipsoriatic; antificanantory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease, AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease,

Homo sapiens.

WO200200928-A2.

03-JAN-2002

02-JUL-2001; 2001WO-EP07537.

30-JUN-2000; 2000DE-1032529. 01-SEP-2000; 2000DE-1043826.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2002-130909/17.

useful Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation

Claim 1; SEQ ID NO 1445; 32pp + Sequence Listing; German.

The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.

Sequence 6106 BP; 1938 A; 30 C; 849 G; 3289 T; 0 other;

Query Match

DB 24; Length 6106; 4.3%; Score 46.2;

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5169 CTAATCAAAACAAATATA-TTCATAAATTAAATTTATAAATACAAATAAAAAA 5111
                                                                                                                                                                                                                                                                                                             156 TITICIAAAAATGICGCTAGTAAAATTTTCAATGGTAGCTCTTGTATCAGCCACAATG 215
                                                                                                                                                                                                                     216 GCTGTAACAACAGTCACACTTGAAAATACTGCACTGGCACGACAAACACAGGTCTCAAAT 275
                                                                                                                                                                                                                                                                               276 GATGTTGTTCTAAATGATGGCGCAAGCAAGTACCTAAACGAAGCATTAGCTTGGACATTC 335
                                            36 TAATTITCATATTITTAAAAAACTATTGATAAACTAGTTAAGTAAGCGTATACTATGG 95
                                                                                                    96 TTAGTTAGCGAAATTAGAAAAGAGGACAAGCATATGAATCTACTTGGATCAAGACGGGTT
                Gaps
                Mismatches 168; Indels
 Pred. No. 0.11;
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48.3%;
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Best Local Similarity
Matches 158; Conserv
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Streptococcus polynucleotide SEQ ID NO 8339.
    BP.
    ABN70213 standard; DNA; 126
             (first entry)
             01-JUL-2002
        ABN70213
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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.

Streptococcus pyogenes

WO200234771-A2.

27-OCT-2000; 2000GB-0026333. 24-NOV-2000; 2000GB-0028727. 07-MAR-2001; 2001GB-0005640. 29-OCT-2001; 2001WO-GB04789 02-MAY-2002.

(CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.

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Fraser

o,

Grandi

Margarit Ros YI,

Masignani V,

Telford J, I Tettelin H;

WPI; 2002-352536/38. P-PSDB; ABP29582.

New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -

Claim 7; Page 3948; 4525pp; English.

The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GAS (Streptococcus/GAS agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory

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activity. (I), mucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) as used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapв
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                                                                                                                                                                                                                                                                                                                                                                                                   4.2%; Score 45; DB 24; Length 126; 100.0%; Pred. No. 0.055; ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACAACGCCTTCTTTTTTCTCCTTACTATCTCCTTTAATTTTCAT 45
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                                                                                                                                                                                                                                                                                                                                                      Sequence 126 BP; 39 A; 12 C; 33 G; 42 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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Search completed: January 5, 2004, 14:01:44 Job time : 354 secs

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California
: USA
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Patent No. 6420152
GENERAL INFORMATION:
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MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Appli Sequence 11, Appli Sequence 11, Appli Sequence 14, Appl Sequence 10, Appl Sequence 12, Appl Sequence 12, Appl Sequence 14, Appl Sequence 14, Appl Sequence 11, Appli Sequence 15, Appl Sequence 11, Appli Sequence 56, Appl Sequence 58, Appl Sequence 58, Appl Sequence 58, Appl Sequence 11, Appl Sequence 58, Appl Sequence 11, Appl Sequence
                                                                                                                                                           ; Search time 92 Seconds
(without alignments)
5195.847 Million cell updates/sec
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Sequence 160, Apr
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                1083
1 GACAACGCCTTCTTTTTCT......TGTGCAAAAAGCAAAAAGC 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2 6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2 6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-393-889-14

PCT-US94-09450-14

US-08-393-889-10

PCT-US94-09450-10

US-08-393-889-12

PCT-US94-09450-12

US-08-323-463-14

US-08-280-590A-36

US-08-280-590A-36

US-08-281-65-11

US-08-281-65-11

US-08-53-63-11

US-08-53-63-11

US-08-887-534A-58

US-08-887-534A-58
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3-09-539-333D-158
3-09-539-333D-160
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                              January 5, 2004, 13:53:48
                                                                                                                                                                                                                                                                                                                                                                               IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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12720
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                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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922.6
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106.6
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                                                                                                                                                              Run on:
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No.
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22	34.4	3.5	999	~	US-08-883-795A-36	Sequence 36, Appl
36	34.4	3.2	4215	4	US-09-620-312D-295	Sequence 295, App
c 31	34.2	3.5	940	4	US-08-393-889-11	Sequence 11, Appl
c 35	34.2	3.5	940	'n	PCT-US94-09450-11	Sequence 11, Appl
c 33	34.2	3.2	1083	4	US-08-393-889-7	Sequence 7, Appl
c 34	34.2	3.2	1083	Ŋ	PCT-US94-09450-7	Sequence 7, Appl
35	34.2	3.2	2235	4	US-09-569-804-20	Sequence 20, Appl
c 36	34.2	3.5	5852	-	US-07-867-106-2	ď
0 37	34.2	3.5	15788	4	US-09-920-759-13	-
c 38	34	3.1	265	4	US-09-016-434-871	871
c 35	34	3.1	1990	4	US-08-961-527-232	Sequence 232, App
c 40	34	3.1	4016	4	US-09-173-053-3	Sequence 3, Appli
. c 41	33.4	3.1	602	-	US-08-764-100-8	æ
4.2	33.4	3.1	642	႕	US-08-764-100-13	Sequence 13, Appl
C 43	33.4	3.1	643	Н	US-08-764-100-7	Sequence 7, Appl
44	33.4	3.1	1257	4	US-09-134-001C-1214	Sequence 1214, Ap
O 64	33.4	3.1	1395	н	US-07-991-867B-25	Sequence 25, Appl
					ALIGNMENTS	
RESULT 1	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2					
-80-SD	US-08-393-889-7					

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Sequence 7, Application US/08393889
Sequence 7, Application US/08393889
Patent No. 6420152
GENERAL INFORMATION:
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Patherina
TITLE OF INVENTION: Streptococcus pyogenes
ITTLE OF INVENTION: Streptococcus pyogenes
CORRESPONDENCE ADDRESS:
ADDRESSES: Sheldon & Mak
STRAES: Saldon & Mak
STRAET: California
COUNTRY: USA
ZIP: 91001
COMPUTER: LBM PC Compatible
OPERATION RYBABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Batter Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE:
CLASSIFICATION NUMBER: US/08/393,889
FILING DATE:
CLASSIFICATION NUMBER: 12,612
REPERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INDER: 312,612
REPERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INDER: 312,612
REPERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INDER: 312,612
REPERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INDER: 9
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1021 TACTAGAAAAAGCAATGATTGCCGTCATTGCTTTTTTATGAATTTGTGCAAAAAAGCAAAAAA 1080
      961 CTCTGCTCACTAGGCCTAGCTTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAA 1020
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                                          1021 TACTAGAAAAAGCAATGATTGCCGTCATTGCTTTTTATGAATTTGTGCAAAAAGCAAAAA
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                                                                                                                                                                                                                                                           ; Sequence 7, Application PC/TUS9409450
; GENBEAL INPORMATION:
; APPLICANT: Beckman Instruments, Inc.
; APPLICANT: 2500 Harbor Boulevard
APPLICANT: Fullerton, California 92634
; TITLE OF INVENTION: Recombinant DNase B Derived from
; TITLE OF INVENTION: Streptococcus pyogenes
; NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1083; DB 5;
100.0%; Pred. No. 7.8e-288;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Beckman Instruments, Inc. STREET: 2500 Harbor Boulevard CITY: Fullerton STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 39D-1357
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-UNN-1993
ATTORNEY/AGENT INFORMATION:
NAME: MAY, William H.
REGISTRATION NUMBER: 26,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1083 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Best Local Similarity 100.
Matches 1083; Conservative
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ADDRESSEE: Beckman I
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129..944
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ORIGINAL SOURCE
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                                                                                                                                                                                                                      RESULT 2
PCT-US94-09450-7
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; LOCATION:
PCT-US94-09450-7
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                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                              ACAAGCATATGAATCTAGGATCAAGACGGGTTTTTTCTAAAAAATGTCGGCTAGTAA 180
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                                                                                                                                                               AATITICAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAA
                                                                                                                                                                                                                  AATTITICAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAA
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                                                           Length 1083;
                                                                                                                                      TCTCCTTACTATCTCCTTTAATTTTCATATT
                                                                                                Indels
                                                       Query Match 100.0%; Score 1083; DB 4; Best Local Similarity 100.0%; Pred. No. 7.8e-288; Matches 1083; Conservative 0; Mismatches 0;
                                                                                                                                    1 GACAACGCCTTCTT
  129..944
LOCATION:
      ;
US-08-393-889-7
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                                                              APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.2%; Score 922.6; DB 4; 99.6%; Pred. No. 7.8e-244; ive 0; Mismatches 4;
                                                                                                                                                                                                                                  ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
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ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
Sequence 11, Application US/08393889
Patent No. 6420152
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FATDET: MICHER B. 2, 612
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6311
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOLECULE TYPE: DNA (genomic)
ANT. CRIT. NO
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 99.6
Matches 925; Conservative
                                                                                                                                                                                                                                                                                                      California
: USA
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STATE: Californi
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                 ZIP: 91001
                                                                                                                                                                                                                                ADDRESSEE:
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     ATTORNEY/AGENT INFORMATION:
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                                            GAAGGTAGCTACGGTGTTAGACAATCTTTCGGTAAAAATCAAAACCCCGCAGGATGGACT
                                                                                                    GGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCGGA
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APPLICANT: 2500 Harbor Boulevard
APPLICANT: 2500 Harbor Boulevard
APPLICANT: 2500 Harbor Boulevard
APPLICANT: NULIerron, California 92634
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAGAAAAGCAATGATTGCCGTCATTGC 1051
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APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
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APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application PC/TUS9409450 GENERAL INFORMATION:
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US94-09450-11
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Pred. No. 7.8e-244;
0; Mismatches 4;
NAME: May, William H.
REGISTRATION NUMBER: 26,769
REFERENCE/DOCKET NUMBER: 39D-1357 PCT
TELECOMMUNICATION INFORMATION:
TELECHONE: (818) 796-4000
TELEPHONE: (818) 795-6321
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 940 base pairs
LENGTH: 940 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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, ORGANISM: Streptococcus pyogenes
PCT-US94-09450-11
                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 99.6%;
Matches 925; Conservative
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963 CTGCTCACTAGGCCTAGCTTTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAATA 1022
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; Sequence 14, Application PC/TUS9409450
; Sequence 14, Application PC/TUS9409450
; Sequence 14, Application:
; APPLICANT: Beckman Instruments, Inc.
; APPLICANT: 2500 Harbor Boulevard
; APPLICANT: Fullerton, California 92634
; TITLE OF INVENTION: Recombinant DNase B Derived from
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.8%; Score 853.8; DB 4;
95.7%; Pred. No. 6e-225;
live 0; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Deriv
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: 18
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 255 South Lake Avenue, Ninth Floor CITY: Pasadena STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                              CTAGAAAAGCAATGATTGCCGTCATTGC 1051
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NET.
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELEPHONE: (818) 795-4000
TELEPAX: (818) 795-4000
INPORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 937 base pairs
LENGTH: 937 base pairs
TYPE: nucleic acid
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Patent No. 6420152
GENERAL INFORMATION:
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Best Local Similarity 95.7
Matches 889; Conservative
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ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 91001
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; LOCATION:
US-08-393-889-14
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                                                                                                                                                                                                                                                                                                                   663 AATGCCGTTACAGGAACACGTACCCAAAATGTAGGAGGTCGTGACCAAAAAGGCGGCATG
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Sequence 10, Application US/08393889
Sequence 10, Application US/08393889
PATENT NO. 6420152
APPLICANT: Adams, Craig W.
APPLICANT: Adams, Patty P.-Y.
APPLICANT: Belei, Marine
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEALER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
COUNTY: USA
ZIPP.
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482
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Pred. No. 6e-225;
0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                      OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-JUN-1993
ATTONEY/AGENT INFORMATION:
INVENTION: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 26,769
RESPERENCE/CONCERT NUMBER: 39D-1357 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 937 base pairs
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 937 base pairs
TERGENCE CHARACTERISTICS:
TERGENCE CHARACTE
                                                                                     E: Beckman Instruments, Inc. 2500 Harbor Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                  ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 95.7%;
Matches 889; Conservative (
                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman I
                                                                                                                                     Fullerton
: California
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                                                                                                            STREET:
CITY: Ful
STATE: Ca
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
                                                                                                                                                                                                                                                                                  Score 200; DB 5; I
Pred. No. 8.9e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CIIY: Pasadena
                                                                                                                                                                                                                                                                                Query Match
18.5%; Score 200; DB
Best Local Similarity 100.0%; Pred. No. 8.9
Matches 200; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AATTTTCAATGGTAGCTCTT 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
  TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 10.
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
COUNTRY: USA
                                                                                                                          linear
                                                                                                                        TOPOLOGY: line
MOLECULE TYPE: I
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91001
                                                                                                                                                                                                                                           PCT-US94-09450-10
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                                                                                                                                                                                                                                                                                                                                       18.5%; Score 200; DB 4; Length 200; 100.0%; Pred. No. 8.9e-46; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SERENT SOUR APPLICATION PC/TUS9409450

GENERAL INFORMATION:
APPLICANT: Beckman Instruments, Inc.
APPLICANT: 2500 Harbor Boulevard
APPLICANT: Pullerton, California 92634
ITLE OF INVENTION: Streptococcus pyogenes
ITLE OF INVENTION: Streptococcus pyogenes
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: 2500 Harbor Boulevard
STREET: 2500 Harbor Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
CLASSIFICATION:
PRIOR APPLICATION UNMBER: US 08/082,845
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: May, William H.
REGISTRATION NUMBER: 26,769
REFERENCE/DOCKET NUMBER: 39D-1357 PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Beckman Instruments, Inc. STREET: 2500 Harbor Boulevard CITY: Fullerton STATE: California
                                                                                                                                                                                                                                                                              ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AATTTTCAATGGTAGCTCTT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AATTTTCAATGGTAGCTCTT 200
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEPAX: (818) 795-631
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 200; Conservative
                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -US94-09450-10
                                                                                                                                                                                                                                                                                                  US-08-393-889-10
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61 TATTGATAAACTAGTTAAGTAAGCGTATACTATGGTTAGCTTAGCGAAATTAGAAAAGAGG 120
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Length 200;
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Patent No. 6420152;
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                 Indels
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SEQUENCE CHARACTERISTICS

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Sequence 904, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-904
                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                oxoaNISM: Synthetic primer
PCT-US94-09450-12
 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 47.3
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGC 182
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                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                             178 TAAAATTTTCAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAAGAGAGTCACAGTTG 237
                                                                                                                                                                                                                                                                                                                                                              61 iraaaricickarddrigerergerriceerakearddergriataeakeerrakeergd 120
                                                                                                                                                                                                                                                                                                                                                                                                238 AAAATACTGGACTGGCACGACAAACACAGGTCTCAAATGATGTTGTTCTAAATGATGGCG 297
                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGGCAATGGATCCGAACCTGCTGGGTTCCCGTCGTTTTCTCCAAAAATGCCGTCTGG 60
                                                                                                                                                                                                                                                           118 AGGACAAGCATATGAATCTACTTGGATGAGGGGGTTTTTTTCTAAAAAATGTCGGCTAG
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                                                                                                                                                                                                 DB 4; Length 182;
                                                                                                                                                                                                                                    Indels
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APPLICANT: 2500 Harbor Boulevard
APPLICANT: 2500 Harbor Boulevard
APPLICANT: 2500 Harbor Boulevard
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
                                                                                                                                                                                    Query Match
9.8%; Score 106.6; DB 4;
Best Local Similarity 77.3%; Pred. No. 3.7e-20;
Matches 143; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRET: 2500 Harbor Boulevard CITY: Fullerton STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39D-1357 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application PC/TUS9409450 GENERAL INFORMATION:
LENGTH: 182 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALECANDA FREAL INFORMATION:
NAME: May William H.
REGISTRATION NUMBER: 26,769
REFERENCE/DOCKET NUMBER: 39D-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 base pairs
TYPE: nucleic acid
                                                                                                                                          Synthetic primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 CAAGC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 CAAGC 182
                                                                                            ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: SYNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                   US-08-393-889-12
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GENERAL INFURNALION:

APPLICANT: LyNn Goucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TILLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TILLE APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-18-14
SEQ ID NOS: 5674
LENGTH: 2409
                                                                                                                                                                                                              178 TAAAATTTTCAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTG 237
                                                                                                                                                                                                                                                     61 TIAAATICHCCAHGGTHGCTCHGGTTTCCGCTACCATGGCTGTTACCACGGTTACCCTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1554 rccraaardicgaccrgcaatraarratraarraraararggritarccrritgaacarag 1613
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                                                                                                                                                           1 Addenatidearcedaactectectederteceteretrirerecanananatecegreres
                                                                                                                                                                                                                                                                                                                  238 AAAATACTGGACTGGCACGACAAACACGGTCTCAAATGATGTTGTTCTAAATGATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 AGGTACATTGACTTATGCCAATGTTGAAGGTAGCTACGGTGTTAGACAATCTTTCGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1434 Addrartrorocardracroarraacaadagaccaaarrigraacroaaaraagagcraa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518 AAATCAAAACCCCGCAGGATGGACTGGAAACCCTAATCATCTCAAATATAAAATTGAATG
                                                                           3;
                      Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2409;
                   DB 5;
                                                                                                       118 AGGACAAGCATATGAATCTACTTGGATCAAGACGGGTTT
Query Match
9.8%; Score 106.6; DB 5
Best Local Similarity 77.3%; Pred. No. 3.7e-20;
Matches 143; Conservative 0; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.4%; Score 47.2; DB 4; 47.3%; Pred. No. 0.0022;
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us-08-482-785-7.rni

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1150 ricaratricricaaaagarraarracragacrararaaaraaaracaraaarca 1091
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                                                                                         686 CCAAAATGTAGGAGGTCGTGACCAAAAAGGCGGCATGCGCTATACCGAACAAAAAGGCTCA 745
    626 CATTGCAGATAGTCTCGGTGGAGATGCACTCAGAGTCAATGCCGTTACAGGAACACGTAC 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 AGCGAAATTAGAAAAGAGGACAAGCATATGAATCTACTTGGATCAAGACGGGTTTTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bodner, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07601

UTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56;
                                                                                                                                                                                                    1089 RRRRRRRRRRRRRRRRRRRRRRATCGCAAGCT 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%; Score 37.4; DB
55.9%; Pred. No. 1.5;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,590A
                                                                                                                                                                          746 AGAATGGTTAGAAGCAAATCGTGATGGCTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-280-590A-36
                                                                                                                                                                                                                                                                                                  US-09-280-590A-36/c

) Sequence 36, Application US/09280590A

; Patent No. 6303772

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 5703 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 29-Mar-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hirai, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                       Inoue, Kazushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.22
Best Tocal Similarity 55.22
Tocal Similarity 55.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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1614 AGACGAAAAAGATTCTCGCTTCGCTAATGAAAGATATCATGCAAATATACAAAATGATGG 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               446 GCGTACTGCTAGAGGTACATTGACTTATGCCAATGTTGAAGGTAGCTACGGTGTTAGACA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     506 ATCTTTCGGTAAAATCAAAACCCCGCAGGATGGACTGGAAACCCTAATCATGTCAAATA 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.2%; Score 45; DB 1; Length 7218; Best Local Similarity 3.8%; Pred. No. 0.014; Matches 15; Conservative 214; Mismatches 164; Indels
                                                                                                                        Sequence 14, Application US/08232463
Fatent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLFOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLSY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-AUG-1991
ATTORNEY/ABENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELECHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
RIOR APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 32313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIVE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAM.
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
FURTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , CLONE: pTZgpt-F18
US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                   Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                           -08-232-463-14/c
                                                                                                                                                                                                                                                                                                                                                                      CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            999
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; TYPE: DNA; CACTOCOCCUS lactis US-09-623-062-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 ACTAGITAAGTAAGCGTATACTATGGTTAGCGAAATTAGAAAAAGAGGACAAGCATA 129
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                                                                                                                                                                               RESULT 14
US-08-134-557D-1/C
i Sequence 1, Application US/08134557D
Sequence 1. Application US/08134557D
GENERAL INFORMATION:
GENERAL INFORMATION:
I APPLICANT: Greene, Marianne E.
APPLICANT: Blumberg, Burce
ITITE OF INVENTION: Receptor Gamma: Compositions and Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, Suite 4700 180 N. Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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3.4%; Score 37.2; DB 3; Length 1844;
Best Local Similarity 50.6%; Pred. No. 1.1;
Matches 90; Conservative 0; Mismatches 88; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRA.

ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/134,557D
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MARTIN. 25,011
REGERENCE/DOCKET NUMBER: 25,011
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1844 base pairs
TYPE: MUCIECI acid
STRANDEDRESS: single
MOLIECITE PROPER
MOLIECITE PROPER
STRANDEDRESS: SINGLE
TOPOLOGY: 11.000
STRANDEDRESS: SINGLE
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; LOCATION: 179..1606
US-08-134-557D-1
   162 AAAAAAT 168
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COUNTRY:
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Sequence 1, Application US/09623062; Patent No. 6448082; GENERAL INFORMATION:

RESULT 15 US-09-623-062-1

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## APPLICANT: PREVOTS, Fabien
## APPLICANT: DALOZAN, MarISne
## TITLE OF INVENTION: DNA Sequences containing a conjugative transfer mechanism
## TITLE OF INVENTION: DNA Sequences containing a conjugative transfer mechanism
## CURRENT PAPLICATION NUMBER: US/09/623,062
## CURRENT PILING DATE: 1999-12-28
## PRIOR PILING DATE: 1999-12-28
## PRIOR PILING DATE: 1999-12-29
## PRIOR PILING DATE: 1999-12-29
## PRIOR PILING DATE: 1999-12-29
## PRIOR PILING DATE: 1999-12-29
## SEQ ID NOS: 23
## SCFTWARE: Patentin Ver. 2.1
## SEQ ID NOS: 23
## SCFTWARE: DALOCOCCUS laction
## SEQ ID NOS: 23
## Score 36-4; DB 4; Length 5333;
## TYPE: DNA
## Score 36-4; DB 4; Length 5333;
## Score 36-4; DB 4; Length 5333;
## Score 36-4; DB 4; Length 5333;
## CONSERVATION OF MARKETHER PARTITION OF OF ORDER PARTITION OF OF ORDER PARTITION OF OF ORDER PARTITION OF OF ORDER PARTITION OF OF ORDER PARTITION OF OF ORDER PARTITION OF OF ORDER PARTITION OF OF ORDER PARTITION OF OF ORDER PARTITION OF OF ORDER PARTITION OF OF ORDER PARTITION OF OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF ORDER PARTITION OF
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Sequence 1447, Ap Sequence 1961, Ap Sequence 146, App Sequence 2170, Ap Sequence 2170, Ap Sequence 644, App Sequence 50, App Sequence 53, App Sequence 53, App Sequence 53, App Sequence 53, App Sequence 1382, App Sequence 1382, App Sequence 2182, App Sequence 2182, App Sequence 275,

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18	US-10-311-4

Sequence 2, Appli Sequence 1822, Ap Sequence 188, App Sequence 228, App Sequence 1299, Ap Sequence 1399, Ap Sequence 1399, Ap Sequence 60, Appl Sequence 2217, App

Sequence Sequence Sequence

ALIGNMENTS

us-08-482-785-7.rnpb

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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: BASE FORM:

COMPUTER: OF PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CORRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/119,900

FILING DATE:

APPLICATION NUMBER: US/09/119,900

FILING APPLICATION

MAMME: PATENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

NAMME: Fatenty MUMBER: 95.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (818) 795-631

INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09119900

Patent No. US20020081622A1

GENERAL INFORMATION:

APPLICANT: Adams, Craig W.

APPLICANT: Belei, Marina

TITLE OF INVENTION: Streptococcus pyogenes

TITLE OF INVENTION: Streptococcus pyogenes

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheldon & Mak

STREET: 225 South Lake Avenue, Ninth Floor

CITY: Pasadena

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 California
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Appli
Sequence 1369, Ap
Sequence 199, App
Sequence 177, App
Sequence 591, App
Sequence 5, Appli
Sequence 1357, Ap
Sequence 1357, Ap
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Sequence 12, Appl
Sequence 1445, Ap
Sequence 2, Appli
                                                                                                                                                                                      January 5, 2004, 14:01:55; Search time 3861 Seconds (without alignments) 970.878 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 GACAACGCCTTCTTTTTTT......TGTGCAAAAAGCAAAAAGC 1083
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Sequence 14
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_MBW_PUB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-311-455-1357

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US-10-311-455-1112
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US-09-119-900-11
US-09-119-900-14
US-09-119-900-10
US-09-119-900-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2263443 segs, 1730637950 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                                                                           US-08-482-785-7
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                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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961 CTCTGCTCACTAGGCCTAGCTTTTTACATCAAAAAGCAATGACTATAGAAAGTAAAAA 1020
                                                                                                                                                                                                                                    1021 TACTAGAAAAAGCAATGATTGCCGTCATTGCTTTTTATGAATTTGTGCAAAAAGCAAAAA 1080
                                                                                                                                                            CTCTGCTCACTAGGCCTAGCTTTTTACATCAAAAAAAGCAATGACTATAGAAAGTAAAAA 1020
                                                                                                                                                                                                                         TATGAATTTGTGCAAAAGCAAAAA 1080
       781 ATTATGAAGTCGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGGTAT 840
                                                                                                901 GCTACACCATTAACTACCATAACGGTACACCTACTCAAAAATAATACCAAAAAGGCTAGAC 960
                                                             Sequence 11, Application US/09119900

Patent No. US20020081622A1

GENERAL INFORMATION:
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from TITLE OF INVENTION: Streptococcus pyogenes

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                      1021 TACTAGAAAAGCAATGATTGCCGTCATTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FAZDEY: MICHAEL B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 940 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                            100.0%; Score 1083; DB 9;
100.0%; Pred. No. 9e-266;
live 0; Mismatches 0;
                                                                                                                                  ORGANISM: Streptococcus pyogenes
              LENGTH: 1083 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 1083; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                CDS
129..944
                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-09-119-900-7
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APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
CORRESPONDENCE: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
FILING DATE:
CLASSIFICATION:
                                                                                                                             ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFRENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPAX: (818) 795-4000
TELEPAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 937 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                            CITY: Pasadena
STATE: California
   GENERAL INFORMATION:
                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                             ZIP: 91001
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                                                                                                                                             ACTGCACTGGCACGACAAAACACACAGTCTCAAATGATGTTGTTCTAAATGATGGCGCAAGC 180
                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                          AAATTAGATGAGTTAGGAAGGACGCGTACTCGCTAGAGGTACATTGACTTGACTTAGACTTATGCCAATGTT 360
                                                                                                                              TITICAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAAAT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGGTAGCTACGGTGTTAGACAATCTTTCGGTAAAAATCAAAACCCCGCAGGATGGACT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCGGA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACACCATTAACTACCATAACGGTACACCTACTCAAAAATAATACCAAAAGGCTAGACCT 962
                                                                                               9
                                                                                     1 ATGGATCCGAATCTAGGATCAAGACGGGTTTTTTTCTAAAAAAATGTCGGCTAGTAAAAA
                                                                                                                                                                                                                                                                              GGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCGGA
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 Length 940;
                                 Indels
 DB 9;
Query Match 85.2%; Score 922.6; DB 9; Best Local Similarity 99.6%; Pred. No. 6.8e-225; Matches 925; Conservative 0; Mismatches 4;
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                                                                                                                                                                     Query Match 78.8%; Score 853.8; DB 9; Length 937; Best Local Similarity 95.7%; Pred. No. 2.4e-207; Matches 889; Conservative 0; Mismatches 37; Indels 3.
ORGANISM: Streptococcus pyogenes PEATURE:
                                                               NAME/KEY:
                                                                                             LOCATION:
                                                                                                                   US-09-119-900-14
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Sequence 14, Application US/09119900 Patent No. US20020081622A1

RESULT 3 US-09-119-900-14

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18.5%; Score 200; DB 9; I
Best Local Similarity 100.0%; Pred. No. 5.8e-41;
Matches 200; Conservative 0; Mismatches 0;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
COUNTRY: USA
ZIP: 91001
MPUTER: USA
ZIP: 91001
                        APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Streptococcus pyogenes
US-09-119-900-10
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
                                                                                              NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEFRAX: (818) 795-6321
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AATTTTCAATGGTAGCTCTT 200
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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AAATTAGATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATGTT
                                                                                                    GAAGGTAGCTACGGTGTTAGACAATCTTTCGGTAAAAATCAAAAACCCCGCAGGATGGACT
                                                                                                                                    GGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATGTTATGTCGGA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
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| Patent No. US20020081622A1
| GENERAL INFORMATION:
| APPLICANT: Adams, Craig W. APPLICANT: Pang, Patty P.-Y. APPLICANT: Belei, Marina TITLE OF INVENTION: Streptococcus pyogenes TITLE OF INVENTION: Streptococcus pyogenes NUMBER OF SEQUENCES: 16
| CORRESPONDENCE ADDRESS: ADDRESSE: Sheldon & Mak
| STREET 225 South Lake Avenue, Ninth Floor CITY: Pasadena CITY: Pasadena CITY: Pasadena CITY: Pasadena CITY: Pasadena CITY: Pasadena CITY: Pasadena CITY: Pasadena COMPUTER: California COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE POSS/SOFFAPING SYSTEM: PC-DOS/MS-DOS/SOFFAPING SYSTEM: PC-DOS/MS-DOS/SOFFAPING SYSTEM: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/SOFFAPINE: PC-DOS/MS-DOS/
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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US-10-312-841-2/c
US-10-312-841-2/c
Sequence 2, Application US/10312841
Publication No. US20030186277A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Disgnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: BO1/1208/WO
CURRENT FILING DATE: 2002-12-30
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
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                      36 TAATITITCATAITITITAAAAAACTATIGAIAAACTAGTIAAGTAAGCGTAIACTAIGG 95
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4.2%; Score 45; DB 13; Length 36
Best Local Similarity 49.8%; Pred. No. 44;
Matches 114; Conservative 0; Mismatches 115; Indels
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ORGANISM: Artificial Sequence
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NAME/KEY: unsure
LOCATION: (379615)
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US-10-311-455-1445/c

1 Sequence 1445, Application US/10311455

1 Publication No. US20030143606A1

1 GENERAL INFORMATION:

APPLICANT: OLEK, APPRICANCK, Christian

APPLICANT: DLEK, APPRICANCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ

TITLE OF INVENTION: Cytosine methylation

TITLE OF INVENTION: Cytosine methylation

FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT APPLICATION NUMBER: PCT/EP01/07537

PRIOR PILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: DE 10043529.7

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR OF SEQ ID NOS: 2424

SEQ ID NO 1445

LEMGTH: 6106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 TAAAATTTTCAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACATTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AAAACACCGCTCTGGC---TCAGACACAGGTCTCAAATGATGTTGTTCTAAATGATGGCG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAATACTGCACTGGCACGACAAACACAGGTCTCAAATGATGTTGTTCTAAATGATGGCG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGGCAATGGATCCGAACCTGCTGGTTCCCGTCGTCTTTCTCCAAAAAATGCCGTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 182;
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4.3%; Score 46.2; DB 13; Length
Best Local Similarity 48.3%; Pred. No. 0.65;
Matches 158; Conservative 0; Mismatches 168; Indels
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ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32 612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELECHONE: (818) 795-4000
TELECKX: (818) 795-400
TELECKX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
LENGTH: 182 base pairs
TYPE: nuclaic acid
TYPE: nuclaic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Synthetic primer
US-09-119-900-12
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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US-10-240-453-199/c
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                 APPLICANT: AKIYANA, YUTAKA
APPLICANT: AKIYANA, YUTAKA
APPLICANT: AKIYANA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
FILE OF INVENTION: GUANGSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT FILING DATE: 2002-11-13
FRIOR APPLICATION NUMBER: 10/017,161
PRIOR PLILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
SOFTWARE PACENTING DATE: 2010-06-18
SOFTWARE PACENTING DATE: 2010-06-18
SOFTWARE PACENTING PACE: 2.1
SEQ ID NO 1369
LENGTH: 744802
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(159571)..(159606)
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(141192)..(141769)
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(174525)..(174575)
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(234891)..(235013)
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(279677)..(279729)
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(409204)..(409669)
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(428381)..(428396)
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(472204)..(472330)
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(744484)..(744602)
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(714447)..(714529)
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(739794)..(739891)
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(27078)..(27094)
SUWA, MAKIKO
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                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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LOCATION:
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LOCATION:
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APPLICANT: DIEX, Alexander
APPLICANT: DIEX, Alexander
APPLICANT: DIEXLIV, Kurt
TITLE OF INVENTION: Diagnostic of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: With DNA TRANScription
TITLE OF INVENTION: With DNA TRANScription
TITLE OF INVENTION: With DNA TRANScription
FILE REFERENCE: 5013.1009
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: DETTERO1/03973
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56341 ACTATTACAAAAGCACTTTCAGATAATAGAAAAACAAGGAACTATATGATTAGCAAACT 56282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56281 GAATTAAACAAATATAAAAAAAAATAACATAACGTATGACCAAGTTGGGTTTATCCTAAAA 56222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
4.0%; Score 43.6; DB 12; Length 744802;
Best Local Similarity 56.2%; Pred. No. 43;
Matches 82; Conservative 0; Mismatches 64; Indels 0; Gaps
NAME/KEY: modified base
LOCATION: (51812). (51911)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                               FEATURE:
NAME/KEY: modified_base
LOCATION: (57122)...(57221)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                           COARTION: (79368)...(79467)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: modified base
LOCATION: (293951)...(294050)
OTHER_INFORMATION: a, t, c, g, unknown or other
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LOCATION: (332935)..(332935)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (332992)
OTHER INFORMATION: a, L, C, G, unknown or other
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LOCATION: (639781)...(639880)

CHER INFORMATION: a, t, c, g, unknown or other

US-10-292-798-1369
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OTHER INFORMATION: a, t, c, g, unknown or other
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Publication No. US20030148326A1
GENERAL INFORMATION:
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NAME/KEY: modified base
LOCATION: (362002)...(362101)
OTHER INFORMATION: a, t, c, g,
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RESULT 12
US-10-311-455-5/c
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Publication No. US20030082609A1

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
TITLE OF INVENTYON: Diagnosis of Diseases Associated with Gene Regulation
TITLE OF INVENTYON: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT APPLICATION NUMBER: PCT/EP01/03968
DE 100190173.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAAAATACTAGAAAAAGCAATGATTGCCGTCATTGCTTTTTATGAATTTGTGCAAAAAG 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7628 icaataaatraaaaatraaaatraaactacaaacaratractaaatarararaaare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

4.0%; Score 43.4; DB 13; Length 8588;
Best Local Similarity 51.9%; Pred. No. 4.1;
Matches 98; Conservative 0; Mismatches 91; Indela n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (4416, 4418, 4430, 4434. 4435, 5243, 5245, 5612)
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; LOCATION: (4416, 4418, 4430, 4434..4435, 5243, 5245, 5612)
US-10-239-676-177
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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2000-06-30
2000-06-30
2000-09-01
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 177
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publication US/10311455

publication US/2030143606A1

publication No. US203030143606A1

publicatur: Dispense No. Contained to the Immune System by Determ

publicatur: BERLIN, Kurt

ritie OF INVENTION: Cytosine methylation

ritie OF INVENTION: Cytosine methylation

ritie OF INVENTION: Cytosine methylation

ritie OF INVENTION: Cytosine methylation

ritie OF INVENTION: UNMBER: US/10/311,455

CURRENT APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR PELING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NO 591

LENGTH: 16373
                                                                                                                                                                                                                                                  CTATTATCTACAACAATAATTAACAAAACCACAAATCTAAACATATCTTAATATATACG 7689
                                                                                                                                                                                                            955 CTAGACCTCTGCTCACTAGGCCTAGCTTTTTACATCAAAAAAGCAATGACTATAGAAAG 1014
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                                                   Indels
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Score 43.4; DB 15;
Pred. No. 4.1;
0; Mismatches 91;
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4.0%; Score 43.4; DB 13;
Best Local Similarity 50.2%; Pred. No. 5.8;
Matches 107; Conservative 0; Mismatches 106;
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Query Match
Best Local Similarity 51.9%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 1521, Application US/10311455
FUDDICATION NO. US20030143606A1
FUDDICATION NO. US20030143606A1
FUDDICATION NO. US20030143606A1
FUDDICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BIEBLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determine TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determine TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determine TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determine TITLE OF INVENTION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02-01
FRIOR FILING DATE: 2001-07-02-02
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR FILING DATE: 2000-09-01
FRIOR FILING DATE: 2000-09-01
FRIOR FILING DATE: 2000-09-01
FRIOR FILING DATE: 2000-09-01
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determa
                                                                                                                                                                                                                                               947 CCAAAAGGCTAGACCTCTGCTCACTAGGCCTAGCTTTTACATCAAAAAAGCAATGACT 1006
                                                                                                                                                                                             887 CAACACAGCTAATGGCTACACCATTAACTACCATAACGGTACACCTACTCAAAAATAATA
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                                                                                                                                                 64;
                                                                                        Score 42.6; DB 13;
Pred. No. 8.4;
0; Mismatches 64;
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Pred. No. 6.8;
0; Mismatches 81;
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Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                            Query Match 3.9%;
Best Local Similarity 55.9%;
Matches 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.9%;
Best Local Similarity 52.9%;
Matches 91; Conservative
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Sequence 1357, Application US/10311455

Publication No. US20030143606A1

Sequence 1357, Application US/20030143606A1

Sequence 1357, Application No. US20030143606A1

SERVERAL INFORMATION:

APPLICANT: PIEBERBRACK, Christian
APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Cycosine methylation
FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT APPLICATION NUMBER: PCT/EP01/0737

FRIOR APPLICATION NUMBER: DE 10032529.7

FRIOR APPLICATION NUMBER: DE 10043826.1

FRIOR APPLICATION NUMBER: DE 10043826.1

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FRIOR APPLICATION NUMBER: DE 10043826.1

FRIOR APPLICATION NUMBER: DE 10043826.1

FRIOR APPLICATION NUMBER: DE 10043826.1

FRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

LENGRIH: 13449
                                                                          APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO S: 2424
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-5
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4.0%; Score 43.2; DB 13;
Best Local Similarity 51.6%; Pred. No. 4.9;
Matches 99; Conservative 0; Mismatches 93;
Sequence 5, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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979 GCTTTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAAATACTAGAAAAAGCAATGA 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

3.8%; Score 41; DB 13; Length 5678;
Best Local Similarity 48.9%; Pred. No. 13;
Matches 110; Conservative 0; Mismatches 115; Indels
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                FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR PILING DATE: 2001-07-02

PRIOR PILING DATE: 2001-07-02

PRIOR PILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-31

NUMBER: DE 10043826.1

NUMBER: PEROF PILING DATE: 2000-09-01

SEQ ID NO 1112

LENGTH: 5678
cytosine methylation
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AZ67711 BX422711
AZ67711 BX722711
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AZ67711 BX722711
BX12771 BX7237569
BH158314 ENTRS42TF
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BK153314 ENTRC139TF
CC082163 CSU-K33T-
BK437758 BX437758
BK13764 BOHEVISTF
BX17553 DANIO FET
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BX277138 DANIO FET
BZ28679 ENTPCG3TR
BX17555 DANIO FET
BX17553 DANIO FET
BX17555 DANIO FET
BX17555 DANIO FET
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BM1345 BCNRUBITR
BX168679 ENTPCG3TR
BH164351 ENTPCG5TR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENTBK82TF
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Sabses 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full_length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr. Web ::www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliangollfetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSIAIO12ZD12QP1.
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11766.539 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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BX462546 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens CDNA clone CSODH003YP10 3-PRIME, mRNA sequence.
/mol_type="mRNA"
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/db xr6f="taxon:9606"
/dlone="CSODIO46YB22"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/dlone_lib="Homos papiens PLACENTA COT 25-NORMALIZED"
/note="ils errand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 187 c 132 g 316 t 109 others
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1 (bases 1 to 1146)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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                                                                                                                                                                                                                                                                         Ouery Match
4.6%; Score 50.2; DB 13; Length 1201;
Best Local Similarity 35.3%; Pred. No. 40;
Matches 174; Conservative 59; Mismatches 260; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
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/clone="CSODHOO3YPIO"
/tissue type="T CELLS (JURKAT CELL LINE)"
/call line="JURKAT CELL LINE"
/call line="JURKAT CELL LINE"
/clone lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/note="Wector: pCWWSPORT 6; lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMWSPORT 6 vector.
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BX456567 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP002XN23
BX456567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BMail: Seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP002CG12NP1.
Location/Qualifiers
                                    For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      996 МАТТТТТТТИМАВАТТТИНАТТТИМУТТТВАВАВАВАТТТТТЯММАМАВАТТ 940
                                                                                                                             Contact
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                                                                                                                 cgi_bin/cluster.cgi?seq=CSODH003DH05NP1&cluster=994.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODH003DH05NP1.
Location/Qualifiers
         a division of
cluster 994.f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 TATGAATCTACTTGGATCAAGACGGGTTTTTTTCTAAAAAATGTCGGCTAGTAAAATT
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Library was constructed by Life Technologies, Invitrogen. This sequence belongs to sequence more information about this cluster, see http://www.genoscope.cns.fr/
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127 c 154 g 436 t
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41.2%; Pred. No. 48;
ative 34; Mismatches
                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSOCAP002YN23"
/tissue_type="THYMUS"
                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
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RESULT 5
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/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(TH) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector.
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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotL-ollgo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
16 c 16 g 59 t 88 others
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BX403499 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA002ZH05
3-PHIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 CTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAAATACTGCACTGGCAC 255
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
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                                                                                                                                                                 Library was not normalized.
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/db_xref="taxon:9606"
/clone="CL0BA002ZH05"
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BX403499.1 GI:30635017
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/mol type="grammic brighter"
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//db_xref="taxon:5821"
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//db_xref="taxon:5821"
//db_bost="Mus musculus"
//lab_bost="Mus musculus"
//lab_bost="Mus musculus"
//lab_bost="Mus musculus"
//note="Wector: pBluescript SK(+) vector DNA, phagemid
excised from lambda ZAP; Site_1: EcoRV; Site_2: EcoRV;
Genomic DNA was prepared from asynchronous blood stage
forms of the cloned ANKA isolate of P. berghei grown in
laboratory Swiss white mice. The DNA was purified from
contaminating host DNA by Hoechst Dye 33258-CsCl
ultracentrifugation and precipitated. Purified DNA was
digested with mung bean nuclease in the presence of 36-38*
formanide at 50 C, as described (Vernick, K.D., Imberski,
R.B. and McCutchan, T.F. 1988 Nucleic Acids Research
16:883-6896. The ends of the digestion fragments were
polished using T4 DNA polymerase, and the fragments size
selected in the range 500-2000 bp. These were ligated into
the EcoRv-cleaved and dephosphorylated pBluescript SK(+)
vector. Recombinant plasmids were used to transform E.
coli Xillo-Gold host cells.
37 a 92 c 51 g 247 t
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                                                                                                                                                                                                                                                                                 70 ACTAGTTAAGTAAGCGTATACTATGGTTAGCGAAATTAGAAAAGAGGACAAGCATA 129
                                                                                                                                                                                                                                                                                                                                                                  130 TGAATCTACTTGGATCAAGACGGGTTTTTTTCTAAAAAATGTCGGCTAGTAAAATTTTTCAA 189
                                                                                                                         10 TICITITICICCTIACTATCTCCTITAATTTTTCATATTTTTAAAAAAACTATTGATAA 69
                                                                                                                                                                                                                                                                                                                                                                                                 627 bp DNA linear GSS 07-MAY-200
MBN #21 Plasmodium berghei genomic 3', genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

[ bases 1 to 627)

[ carlron,J.M.-R. and Dame, J.B.

The Plasmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)

Contact: Dame JB

Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 387 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA

Fax: 352 392 4700
                                                                 Gaps
                                                                 ó.
      Length 427;
                                                              Indels
                                                                 73;
      DB 13;
      ch 4.5%; Score 48.2; DB 13
.1 Similarity 32.2%; Pred. No. 1.2e+02;
59; Conservative 51; Mismatches 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: damej@mail.vetmed.ufl.edu
Seq primer: M13(-20) forward
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Class: shotgun.
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213PbB09 Pb
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/tissue type="NEDROBLASTOMA"
/clone lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(TI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and cloned into the Not I and cloned into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 15-MAY-2003
                                                                                                                                                                                                                                                                                                           70 ACTAGTTAAGTAAGCGTATACTATGGTTAGCGAAATTAGAAAAGAGGACAAGCATA 129
                                                                                                                                                                                                                                                           222 TITINITITITITITITITITITITITITAATAGITITAATGIATITAATAAATTITAATAAACA 163
                                                                                                                                                                                                                                                                                                                                                               162 TARATTARATTATTARARATTATTATTACGTTTCTACATTTACARARGAAAATGTT 103
                                                                                                                                                                                                                                                                                                                                                                                                                  130 TGAATCTACTTGGATCAAGACGGGTTTTTTCTAAAAATGTCGGCTAGTAAAATTTTCAA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 İCTTİTİĞİRİZAĞAİTAATTATĞITİTCATTATATAAAAGCAATAAİTCCAAAAİTİTİĞAĞ 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo. Li, W.B., Gruber, C., Jessee, J., and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Context: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODAOllBEO7QP1.
Location/Qualifiers
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BX416727 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CSODA011Y114 5-PRIME, mRNA sequence.
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11.5%; Pred. No. 1.6e+02;
                                                                                                         DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Pred. No. 2.2e+02
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library is possible."
18 c 20 q
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/db_xref="taxon:9606"
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                                                                                                      4.4%;
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The library was constructed by Brandi Chiapelli and Dr.
James McCarter at Washington University, St. Louis. The
CDNA was made by using Dynabead oligo-dT priming (Dynal).
PCR based library using a modified protocol from the
SMART PCR CDNA Synthesis Kit from Clontech. Directionally
cloned into the UDG sites of pAMP1. Nematodes were
provided by Dr. Warwick Grant of AGRearch, New Zealand
(warwick.grant@agresearch.co.nz). Worms were harvested
from Australian brush-tailed possum (Trichosuri vulpecula
) and washed thoroughly to remove host contamination.
Note that despite this effort, host contamination of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bl/43690 254 bp mRNA linear EST 25-SEP-2001 kx50f04.yl Parastrongyloides trichosuri PA pAMP1 vl Chiapelli McCarter Parastrongyloides trichosuri cDNA 5', mRNA sequence. Bl743690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tengarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
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                                                                                                                                                                                                                          89 ACTATGGTTAGTTAGGAAATTAGAAAAGAGGACAAGCATATGAATCTACTTGGATCAAG 148
                                                                                                                      Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu)
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Seq primer: -40RP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                              319 ATTTATATTAACAAAAAGAAATAAGTAAATAATAATGGCATCAAACATTTTGTTCGAAG
                                                                           Gaps
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Chiapelli McCarter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parastrongyloides trichosuri
Parastrongyloides trichosuri
Ebkaryota; Metazoa, Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Parastrongyloides.
                        Length 627;
                                                                        Indels
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/mol_type="mRNA"
/db_xref="taxon:131310"
                                                                                                                                                                                                                                                                                                                                 149 ACGGGTTTTTTCTAAAAATGTCGGCTAGTAAAATTTTCAA 189
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                     4.4%; Score 47.4; DB 28; 55.9%; Pred. No. 1.5e+02;
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lab_host="DH108"
                                                                      0; Mismatches
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AZ691287 14-DEC-2000 BNTWC74TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                        CTCTGCTCACTAGGCCTAGCTTTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAAA 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3543
Tel: 301 838 3543
Tel: 501 Joftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                   271 MMMAAMWCRAAWMGGAWARAAWTRGAWWAWRAWMAAARAARAARAARAARAAWAAAWAAAW 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTACACCATTAACTACCATAACGGTACACCTACTCAAAAATAATACCAAAAGGCTAGAC 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 881)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
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/mol_type="genomic DNA"
/strain="HM1:IMSS"
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Pred. No. 1.7e+02;
0; Mismatches 102;
                                                                                                                                                 1021 TACTAGAAAAGCAATGATTGCCGTCAT 1048
                                                                                                                                                                                       331 TACAWAAAWAAARTMRTAWGMAGAAAT 358
                                                                                                                                                                                                                                                                                                                         genomic, genomic survey sequence. AZ691287
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High quality sequence stop: 822.
Location/Qualifiers
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Entamoeba histolytica
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Best Local Similarity 51.4%;
Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-3011-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                              781 ATTATGAAGTCGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGTT 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGATGGCTATCTTTATTATGAAGTCGCTCCAATCTACAACGCAGACGAGTTGATTCCAA 825
                                     91 АМАМАААМАМИМААААААМИМАМАКСАМАКСИМССИМССАНИМИМИМИКСИМИМИМИМИАМИАААА 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                     o.o by UNA linear GSS 26-JUL-19
BACN04E04 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                                                            GAGCTGTCGTCGTATCAATGCAATCTTCTGATAATACCATCAACGAGAAAGTATTAGTTT
                                                                                                                                                   886 ACAACACAGCTAATGGCTACACCATTAACTACCATAACGGTACACCTACTCAAAAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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1 Similarity 24.6%; Pred. No. 1.7e+02;
66; Conservative 85; Minnot-Lander
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/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
/clone="BACN04E04"
/clone_lib="DrosBAC"
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Best Local
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Matches
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CNS0187R
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/MOI_type="genomic DNA"
/#Carain="HM1:IMSS"
/db_rate="uscon:5759"
/db_rate="uscon:5759"
/doine lib="Entamoba histolytica Sheared DNA"
/clone lib="Entamoba histolytica Sheared DNA"
/note="Vector: pHOSI; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.; The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, u h and very library construction is described in detail in Smith,
                                                                                                                           972 YWTITITKKRGKGGVVVVRSGSBVSANSGVRRARVGAGGDATWAAAAAASASADAWAWA 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH132872 885 bp DNA linear GSS 07-AUG-2001
ENTNU65TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
7912 Medical Center Dr., Rockville, MD 20850, USA
7913 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                   194 AGCICITGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAAATACTGCACTGGC 253
              912 KATASKGTGTATWAAAMAGAAHTATWTWTAKWWTAWATATWTRWADAAAARKTWATRTA 971
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Entamoeba histolytica
Entamoebidae; Entamoeba.

1 (bases 1 to 885)
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:MSS sheared DNA library (2001)
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                                                                                                                                                                                                                                                                 Score 46.4; DB 28; Length 885;
Pred. No. 2e+02;
0; Mismatches 96; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic, genomic survey sequence.
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High quality sequence stop: 667.
Location/Qualifiers
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Seg primer: M13-Reverse
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Best Local Similarity 52.0%;
Matches 104; Conservative
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BH132872
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- Web : www.genoscope.cns.fr

- Ollaboration with the Barkeley Drosophila Genome Project

collaboration with the Barkeley Drosophila Genome Project

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Gosegawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

Pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPG Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 04-JUN-1999
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                                                                                                                                                    213
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                                                             Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
94 GGTTAGTTAGCGAAATTAGAAAAGAGGACAAGCATATGAATCTACTTGGATCAAGACGGG 153
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LOS 04-JUN-19
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR28118 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                      154 ITITITCTAAAAATGTCGGCTAGTAAATTTTCAATGGTAGCTCTTGTATCAGCCACAA
                                                                                                                                                                                                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila,
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Location/Qualifiers
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|mol_type="genomic DNA"
|db_xref="taxon:7227"
                                                                                                                                                                                                                                                                            214 TGGCTGTAACAACAGTCACACTTGAAAATA 243
                                                                                                                                                                                                                                                                                                                              596 ATAAATAAGAAAGATAAGACTGAATAAGA 567
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/note="end : T7"
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Best Local Similarity 30.2°
Matches 88; Conservative
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lste fixand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
36 a 79 c 211 g 264 t 251 others
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4553.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS1A1014ZC08NP1&cluster=4553.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://filllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1A1014ZC08NP1.
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BX344084 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI054YA14 3-PRIME, mRNA sequence.
                                  164 AAAATGTCGGCTAGTAAAATTTTCAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAAC 223
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                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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                                                                                                                                         186 AAAGATAAGACTGAATAAGA 205
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                                                                                                    224 AACAGICACACTIGAAAIA
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/tissue type="INDROBLASTOWA"
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/clone_lib="Homo sapiens NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
//thote="Vector: pCMVSPORT_6" ist strand cDNA was primed
/with a NorI-oligo(dT) primer. Five prime end enriched,
/double-strand cDNA was digested with Nor I and cloned into
Library was not normalized."
// 227 c 206 g 559 t 148 others
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AATGATGGCGCAAGCAAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCT 347
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Li M.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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cgi.bin/cluster.cgi?eeq=CL0BB010Z602FP1&cluster=10024.f. Contact
cgi.bin/cluster.cgi?eeq=CL0BB010Z602FP1&cluster=10024.f. Contact
berg Liang Email: fliangelifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CL0BB010Z602FP1.
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedax - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10024.f f
more information about this cluster, see
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40.2%; Pred. No. 2e+02;
iive 31; Mismatches 94; Indels 0
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Genoscope - Centre National de Sequencage
BP 191 91006 BYRY cedex - France
BFmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO18BD12QP1.
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8X356851 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens CDNA
Clone CSODIO18YG24 5-PRIME, mRNA sequence.
BX356851
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BX436282 .
BX436282.1 GI:30787521
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1. ("B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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4.3%; Score 46.2; DB 13; Length 1201;
Best Local Similarity 27.6%; Pred. No. 2e+02;
Matches 63; Conservative 65; Mismatches 100; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       031 AGCAATGATTGCCGTCATTGCTTTTATGAATTTGTGCAAAAAGCAAA 1078
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                                                                                                                                                                                                                                                                                                     BX356851.1 GI:30368066
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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   264
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                                                                                                                                                                                                DEFINITION
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VERSION
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AUTHORS
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KEYWORDS
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Homo sapiens (human) Homo sapiens

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/clone=CSOCARDOLYCOL"
/tissue Lype="THYMUS"
/clone_lib="Homo sappens THYMUS"
/clone_lib="Homo sappens THYMUS"
/note="Tel="The" primer. Five prime end enriched,
with a Not1-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECCRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
a 29 c 109 g 435 t 422 others
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                                                                                                                       Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: filangalifetech.com URL:
http://full.langth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAPO01AB01QP1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1124;
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                  Mammalia, Butheria, Primates, Catarrhini, Hor
1 (Dases I to 1124)
Li W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
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llarity 23.6%; Pred. No. 2.4e+02;
Conservative 116; Mismatches 169;
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Job time: 2245 secs
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JOURNAL
COMMENT
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AUTHORS
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Matches
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Streptococcus poly Group B Streptococ

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Lretteri linoleat
Streptococcus poly
Linoleate isoneras
Lretteri linoleat
Streptococcus poly
Streptococcus poly
Streptococcus pneu
S. pneumoniae type
C. histolyticum cl
S. pyogenes DNaseB
C. ditamicum prote
H. pylori outer me
H. pylori outer me
H. pylori outer me
H. pylori outer me
H. pylori outer me
H. pylori outer me
Straphylococcus poly
Streptococcus poly
Straphylococcus epi
Straphylococcus epi
Straphylococcus epi
Straphylococcus epi
Trichoderma reesei
Trichoderma reesei

Perfect score:

Sequence:

protein

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Run ĕ

Scoring table:

rotal number Minimum DB E Maximum DB E

Database

Searched:

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Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine, meningitis; gene therapy.
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ABP27393
ABP25596
ABP25596
ABP27392
ABP29813
ABP29813
ABP29813
ABP20612
AAX22337
AAX22337
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AAX22333
ABP27570
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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(GENO-) INST GENOMIC RES
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  Streptococcus pyogenes
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  Streptococcus poly DNA-ase-B. Strept S. pyogenes DNaseB Mitogenic factor a Recombinant DNA-as DNA-ase-B2 N-termi S. pyogenes DNase Leader peptide. S Recombinant DNaseB
                                                                                                                                   ; Search time 69.8711 Seconds (without alignments) 615.632 Million cell updates/sec
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                                                                                                                                                                                                                                                          MNLLGSRRVFSKKCRLVKFS.....VYNTANGYTINYHNGTPTQK 271
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                                                                                                                                                                                                                                                                                                                                                                                                             1107863
              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                     of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                 1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                               - protein search, using sw model
                                                                                                                                        2004, 15:08:48
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AAR80823
AAR80823
AAR58702
AAR70701
AAR70700
AAR80822
AAR88822
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
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                                                                                                                                        January
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Match
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Wild-type Staphylo Escherichia coli F Bacillus sp. AA386

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Result ò

Trichoderma reesei Trichoderma reesei Trichoderma reesei Trichoderma reesei

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/note= "leader peptide: claim 11"
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                                                                                                                                                      (BECI ) BECKMAN INSTR INC.
                                                                                                                                                                               Adams CW, Belei CM,
                                                                                                                                                                                                       WPI; 1995-052087/07
                                                                                                                                                                                                                                                                                                                                                                                                  293 AA;
                                                                                                                                                                                                                     N-PSDB; AAQ85037
             misc_difference
                                                                                                     18-MAY-1994;
                                                                                                                              23-JUN-1993;
                                                   WO9500650-A1
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                                                                             05-JAN-1995
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                                                                                                                          treptococcus yogenes), comprising one of 5483 sequences (Streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the proteins have antibacterial and antihitlammatory activity. (I), nucleic acids encoding (I), ABM66044-ABM71526 and antihitlammatory cartivity. (I), nucleic acids encoding (I), ABM66044-ABM71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly salalaties and S. Pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to biological sample. (I) is used to determine whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRIRTARGTLTYANVEG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYGVRQSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                       o Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and catecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNLLGSRRVFSKKCRLVKFSMVALVSATWAVTTVTLENTALARQTQVSNDVVLNDGASKY
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                   The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                        99.7%; Score 1414; DB 23; Length 271; 99.6%; Pred. No. 3.5e-138; ive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-ase-B; diagnostic; vaccine; cystic fibrosis therapy
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46..293
/note= "mature protein"
1..45
                                                                                             Claim 1; Page 4045; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pyogenes (ATCC 14289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR70702 standard; Protein; 293 AA
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.6
Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                           Streptococcus proteins.
      WPI; 2002-352536/38
                                                                                                                                                                                                                                                                                                                                                    271 AA;
                  N-PSDB; ABN70648
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YGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 NLIGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 NEALAWIFUDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence shows a gene product corresponding to a Streptococcus pyogenes DNA-ase-B. The protein is useful as a diagnostic agent, accine or as an aerosol to trea excessive lung viscosity, e.g. in cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA encoding Streptococcus pyogenes DNase B - for diagnosing
S. pyogenes infection, also new promoter for expressing other
proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNase B; nuclease; cystic fibrosis; vaccine; immunoassay; diagnosis; Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Match 99.6%; Score 1413; DB 16; Local Similarity 100.0%; Pred. No. 5e-138; tes 270; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Updated on 25-MAR-2003 to correct PN field.)
/note= "in-frame stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDNTINEKVLVYNTANGYTINYHNGTPTQK 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. pyogenes DNaseB and leader sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 5; 97pp; English.
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61 63 121 123 181 241 243

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61 LNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNEALAPTENDSPNYYKTLGTSOITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AARS8702 shows a mitogenic factor which exhibits rabbit peripheral blood lymphocyte mitogenicity and/or DNA hydrolysing activity. It is strongly associated with group A Streptococci and the nucleotide sequences can be used for the microdetection of the gene and provide an early diagnosis of infectious disease caused by the bacteria. (Updated on 25-MAR-2003 to correct PN field.)
                                   mitogenic factor; microdetection; group A streptococci; spe; erythrogenic toxin; streptococcal pyrogenic exotoxin; blastogens; scarlet fever toxin; erythematous skin reaction; infectious disease;
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                                                                                                                                                                                                                                                                                                                                                              Kishishita M;
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Mitogenic factor associated with group A Streptococci.
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                                                                                                                                                                                                                                                                                                                                                              Iwasaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSDNTINEKVLVYNTANGYTINYHNGTPTOK 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 12-13; 20pp; English.
                                                       erythrogenic toxin, streptococcal
scarlet fever toxin, erythematous
delayed hypersensitivity, ss.
                                                                                                                                                                                                                                                                                                                                                                                Yutsudo T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR70701 standard; protein; 229
                                                                                                                                                                                                                                                                                                                                                              Hinuma Y, Igarashi H,
K, Takeda Y, Yutsudo
                                                                                                                                                                                                                                                  94EP-0101386.
                                                                                                                                                                                                                                                                                                                        (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 98.5
Matches 267; Conservative
                                                                                                                                 Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-272994/34.
N-PSDB; AAQ71612.
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                                                                                                                                                                                                                                                31-JAN-1994;
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Okumura K,
                                                                                                                                                                     EP613947-A2
                                                                                                                                                                                                            07-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYGVROSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYGVROSFGKNONPAGWIGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 INEALAWIFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRIRTARGTLTYANVEG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes DNase B, including the leader peptide, has the amino acid sequence given in AAR8881. The enzyme can be obtd. on a large scale by expression of encoding DNA (AAI12774) in transformed host calls, esp. Escherichia coli. Inclusion of the leader peptide facilitates purification of the recombinant enzyme. The DNase B is useful in immunoassays to detect anti-DNase B antibodies in serum as a marker for S. pyogenes infection, and is also useful as a vaccine or for treatment, via aerosol delivery, of cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding Streptococcus pyogenes DNase B - for recombinant
dn. of the enzyme in other bacteria, useful in immunoassays or
treating cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1412; DB 17;
Pred. No. 5.6e-138;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..43
/label= Sig_peptide
                                                     /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 67-70; 115pp; English
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AARS8702 standard; Protein; 271 AA.
                                                                                                                                                                                                                                                                                                       Pang PPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 99.6%;
Local Similarity 99.6%;
les 270; Conservative
                                                                                                                                                                                        94WO-US09450
                                                                                                                                                                                                                            94WO-US09450
                                                                                                                                                                                                                                                               (BECI ) BECKMAN INSTR INC.
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(first entry)
                                                                                                                                                                                                                                                                                                     Belei MC,
                                                                                                                                                                                                                                                                                                                                      WPI; 1996-151377/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 AA;
                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT12774.
                                                                                                                                                                                                                            18-AUG-1994;
                                                                                                                                                                                       18-AUG-1994;
                                                                                                              WO9606174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
29-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                       prodn. of
                                                                                                                                                                                                                                                                                                       Adams CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR58702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
Key
Peptide
                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                   New
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1 MNLIGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY
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                                                                                                                                                                                                                                                                                   New DNA encoding Streptococcus pyogenes DNase B - for diagnosing S. pyogenes infection, also new promoter for expressing other proteins
                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents the N-terminal fragment of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                     pyogenes DNA-ase-B, which is a marker of S. pyogenes infection. The protein may be used as a diagnostic agent or vaccine for S. pyogenes, or may be used as an aerosol to treat excessive lung viscosity, e.g. in Cystic fibrosis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNase B; nuclease; cystic fibrosis; vaccine; immunoassay; diagnosis; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.2%; Score 456; DB 16;
100.0%; Pred. No. 2.2e-39;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LNEALAWTFNDSPNYYKTLGTSQITPALFPK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNEALAWTFNDSPNYYKTLGTSQITPALFPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes strain ATCC 14289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S. pyogenes DNase B partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR88821 standard; Protein; 90 AA
                                                                                                                                                                                                               PPY;
                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 3; 97pp; English.
                                                                                               94WO-US05626
                                                                                                                                    93US-0082845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                               Adams CW, Belei CM,
                                                                                                                                                                                                                                                  1995-052087/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 AA;
                                                                                                                                                                                                                                                                 N-PSDB; AAQ85036
                                                                                                                                    23-JUN-1993;
                                                                                                 18-MAY-1994;
                       WO9500650-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9606174-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-AUG-1994;
                                                            05-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR88821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               음
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the full-length sequence of Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-ase-B, which is a marker of S. pyogenes infection. The prote may be used as a diagnostic agent or vaccine for S. pyogenes, or may be used as an aerosol to treat excessive lung viscosity, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA encoding Streptococcus pyogenes DNase B - for diagnosing S. pyogenes infection, also new promoter for expressing other proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIXNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTFTQK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.0%; Score 1220; DB 16; Length 229; 100.0%; Pred. No. 3.8e-118; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-ase-B2 N-terminal fragment; diagnostic; vaccine; cystic
                                                                              vaccine; cystic fibrosis therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in cystic fibrosis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR70700 standard; Protein; 91 AA
                                                                                                                                                                                                                                                                                                                                            Pang PPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-ase-B2 N-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 4; 97pp; English.
                                                                                                                                                                                                                            94WO-US05626
                                                                                                                                                                                                                                                               93US-0082845
(first entry)
                                                                                                                                                                                                                                                                                                    (BECI ) BECKMAN INSTR INC.
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(first entry)
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                                                                            DNA-ase-B; diagnostic;
                                                                                                                 Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes
                                         DNA-ase-B.
                                                                                                                                                                                                                                                                                                                                          Belei CM,
                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-052087/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrosis therapy
                                                                                                                                                  WO9500650-A1
                                                                                                                                                                                                                          18-MAY-1994;
                                                                                                                                                                                                                                                               23-JUN-1993;
 14-AUG-1995
                                         Recombinant
                                                                                                                                                                                         05-JAN-1995
                                                                                                                                                                                                                                                                                                                                          Adams CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Gaps

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Indels

Length 91;

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AAR88823) in transformed bacterial hosts, e.g. Escherichia co
The leader peptide can also be used for expression and prodn.
of other recombinant proteins in bacteria. The product is
excreted by the host into the culture medium and is easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams CW, Belei MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-151377/15
                                                                                                   Best Local Similarity
                                                                    43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 AA;
                                                                                                                                                                                                                                                                                                                                                                  WO9606174-A1
                                                                                                                                                                                                                                                                                                                                                                                                               18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                    18-AUG-1994;
                                                                                                              43;
                                                                                                                                                                                                                                                              25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                        29-FEB-1996
                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                recovered
                                                                    Sequence
                                                                                                                                                                                                                                         AAR88825;
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                                                                                         Query Match
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ABP27393
                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                       MILLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY
                                                                                                                                                                                                                                                                                                          1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                 is the product of DNA clone lambda 2-6 (AAT12773) isolated from a S. pyogenes DNA library. A full-length sequence is given in AAR8823. The insert of the DNase B-encoding DNA clone can be transferred to expression plasmids for large-scale recombinant DNase prodn. in E. coli or other bacterial hosts. It is used in mannoassays to detect anti-DNase Banthodies in serum as a marker of S. pyogenes infection, and is also useful as a vaccine or for cystic fibrosis treatment via aerosol delivery.
                                                       New DNA encoding Streptococcus pyogenes DNase B - for recombinant prodn. of the enzyme in other bacteria, useful in immunoassays or for treating cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA encoding Streptococcus pyogenes DNase B - for recombinant prodn. of the enzyme in other bacteria, useful in immunoassays or for treating cystic fibrosis
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                                                                                                                        A partial sequence (AAR88821) for Streptococcus pyogenes DNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A leader peptide (AAR88822) of Streptococcus pyogenes DNase E
can be used to facilitate prodn. of recombinant DNase B (see
                                                                                                                                                                                                                                                              Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNase B; nuclease; cystic fibrosis; vaccine; immunoassay; diagnosis; leader peptide.
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                              Score 451; DB 17;
Pred. No. 7.2e-39;
                                                                                                                                                                                                                                                     31.8%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      61 INEALAWTFNDSPNYYKTLGTSQITPALFP 90
                                                                                                                                                                                                                                                                                                                                                                      LINEALAWTENDSPNYYKTLGTSQITPALFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes strain ATCC 14289
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR88822 standard; Peptide; 43 AA
                                                                                                  Example 2; Fig 3; 115pp; English.
  Pang PPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pang PPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US09450
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Best Local Similarity 100.
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BECI ) BECKMAN INSTR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Belei MC,
Belei MC,
                      WPI; 1996-151377/15.
N-PSDB; AAT12773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-151377/15.
                                                                                                                                                                                                                                        90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9606174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-AUG-1994;
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 Adams CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prodn. of
                                                                                                                                                                                                                                        Sequence
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                                                      New DNA
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                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The N-terminal sequence (AAR88825) of a Streptococcus pyogenes recombinant DNase B expressed in Escherichia coli transformants was detd. A modified DNase B gene (AAT12780) was produced by PCR amplification of the native DNase B gene (AAT12774) in clone lambda The gene was inserted into vector del-33 for expression in E. coli. Modification of the gene resulted in the presence of an additional Arg residue at the DNase B N-terminus (see also AAR88824).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding Streptococcus pyogenes DNase B - for recombinant prodn. of the enzyme in other bacteria, useful in immunoassays or for treating cystic fibrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNase B; nuclease; cystic fibrosis; vaccine; immunoassay;
                                                     Indels
14.3%; Score 203; DB 17; Length 100.0%; Pred. No. 1.3e-13; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                      43
                                                                                                                                                         43
                                                                                                                                         MILIGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR
                                                                                                      1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 202; DB
100.0%; Pred. No. 1.4
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNaseB N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 48; 115pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pang PPY;
                                                                                                                                                                                                                                                                                          AAR88825 standard, Peptide; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-US09450.
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 38, Conservative
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ABP27393 standard; Protein; 252

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RESULT 11
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                                                                                              Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 ITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGSYGVRQSFGK-NQNPAGWTGNPN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 LLP--FTANYQLQLGELDNLN----RATFSHIQLQDRHETKDVRTKINYDPVGW---- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HVKYKIEWING--LSYVGDFWNRSHLIADSLGG--DALRVNAVTGTRTQNVG---GRDQK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                    New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 LVSATMAVTIVTLENTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.9%; Score 182.5; DB 23; Length 252; 24.6%; Pred. No. 2.8e-10; Live 48; Mismatches 93; Indels 67;
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                                                                                                                                                                                                                                                                                                                                    Grandi
                                                                                                                                                                                                                                                                                                                              Masignani V, Margarit Ros YI,
                                                                         Streptococcus polypeptide SEQ ID NO 3962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 3550; 4525pp; English.
                                                                                                                                                                                                                                                      24-NOV-2000; 2000GB-0028727.
                                                                                                                                                                                                                                             27-OCT-2000; 2000GB-0026333.
                                                                                                                                                                                                                    29-OCT-2001; 2001WO-GB04789
                                                  (first entry)
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                                                                                                                                                                                                                                                                                           (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
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                                                                                                                                               Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-352536/38.
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les 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 AA;
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                                                                                                                                                                      WO200234771-A2.
                                                02-JUL-2002
                                                                                                                                                                                                                                                                                                                              Telford J,
Tettelin H;
                                                                                                                                                                                               02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Best Local S
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101 H-NYQFPYGDGSKSSWV---MNRGHLVGYQFCGLNDEPR-NLVAMTAWLNTGAYSGANDS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
group A streptococcus; Streptococcus pyogenes; antibacterial;
antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grandi G,
                                                      196 G--GMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAV-
                                                                                                                                                                                  216 NSNKESIDENGVITVILENSAPNINLDYLNGTATPK 251
                                                                                                                                                    240 QSSDNTINEK----VLVYNTANGYTINYHNGTPTQK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus polypeptide SEQ ID NO 368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 3190; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                      ABP25596 standard; Protein; 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2002 (first entry)
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(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Telford J, Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-352536/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABN66227
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                                                                                                                                                                                                                                                                                                                                                                                       ABP25596;
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and activity and that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Streptococcus and particularly S. agalactiae and S. pyrogenes. Streptococcus ample. (I) is used to detect Streptococcus in a biological sample. (I) is used to detectine whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Used as a vaccine or diagnostic composition. The disease caused by a streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity strentoccus in a proper antibodies to (I) are used for affinity strentoccus in a processing that is prevented or treated may be negative to acid encoding (I) and may be a promatography, immunoassays, and distinguishing/identifying Streptococcus proteins.

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268 AA; Sequence

Query Match

11.4%; Score 161.5; DB 23; Length 268;

TDNSSQVSTKSLASSVKQAPLTFKNQRQMVMANTDALGRAVDSHIQLKDSQEPKVKREPL 98

39

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102 PGW-----H-NYKLTDANGKT----TWLMDRGHLVGYQFSGLNDEPK-NLVTWTKYLNTG 150
                                                                                                                       81 TSQITPALFPKAG--DILYSKLDELGRTRTARGTLTYANV----EGSYGVRQSFGKNQNP 134
                                                                                                                                                54 ----TPGILPFFTGSYQLVLGDLDNLQRP------TFAHIQLKDQDEFNIKRK-GLKFNP 101
                                                                                                                                                                                           135 AGWTGNPNHVKYKIEWLNGLSYVGDFW--NRSHLIADSLGG--DALRVNAVTGTRTQNVG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           frequence (ARA90521) and related proteins (ARB55021). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent WO200177314 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                    21 MVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 80
                                                                                                                                                                                                                                                                                    New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention is related to a Lactococcus lactis nucleotide
                                                                                                                                                                                                                                                              191 GRDOKG-GMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 153.5; DB 23; Length 263; 24.4%; Pred. No. 3.1e-07; ive 26; Mismatches 85; Indels 75;
                   83; Indels
                                                                         :| |::
15 VVILIAILTTFTTSTVTAARKIRNFPDTTEILLGTKATE-
   Pred. No. 4.7e-08;
5; Mismatches 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID No 162; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Renault P,
                                                                                                                                                                                                                                                                                                                                                                                     ABB53460 standard; Protein; 263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis protein ybfB.
 larity 25.6%; Pr
Conservative 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sorokine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-043418/06.
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-2002
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streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5481 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), AM86044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to li). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic
                                                                      169 DSLGGDALRV-----NAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYY 219
                                                                                                                                                                    SGLNNEARNLVPETAWFNGGNFTGTNDGNT----ASMLYYENRLDSWLANHPNYYLDY 189
   114 TYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFW--NRSHLIA--- 168
                                 TY-------NPVGW-----H-NYNFYYKKSDGSIGKMWLMARGHLVGYQF 135
                                                                                                                                            EVAPIYNADELIPRAV---VVSMQSSDNTINEK--------VLVYNTANGYTI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial, antiinflammatory, infection, vaccine, meningitis, gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masignani V, Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus polypeptide SEQ ID NO 3960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 3550; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                           ABP27392 standard; Protein; 354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus agalactiae
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N-PSDB; ABN68023.
                                                                                                                                                                                                                   NYHNGT 267
                                                                                                                                                                                                                                                    NYADGT 255
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Tettelin H;
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68 TFNDSPNYYKTLGTS-QITPALFPKAGDILYSKLDELGRT

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Best Local Similarity 24.4 Matches 60; Conservative

Query Match

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268 PTQ 270
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                                                                                                                                                                                          Sequence
                                                                                                                                                                                                              Query Match
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                                                                                                                                                   67 WIPNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRIRTARGTLTYANVEGSYGVRQ 126
                                                                                                                                                                                         127 SFGKNQ-----NPAGWTGNPNHVKYKIEWLNGLSYVGDFW--NRSHLJADSLGG-DALR 177
                                                                                                                                                                                                                                 VNAVTGTRTQNVGGRDQKG-----GMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIP 232
                                                                                                                    99
                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial, antiinflammatory, infection, vaccine, meningitis, gene therapy.
                                                                                                           7 RRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALA
                                                                                                                                                                 may be
                                                                                                                                                                                                        3 KKQFIKLGIATLLTVISLYTPINLATNHTTENIVTAQE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                     83;
acid encoding (I) may be used to recombinantly produce (I) and used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.
                                                                        DB 23; Length 354;
                                                                                                                                                                                                                                                                        RAVVVSMQSSDNT-----INEK-----VLVYNTANGYTINYHNG
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                                                                                              Indels
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                                                                                 ; Pred. No. 1.8e-05; 40; Mismatches 103;
                                                                       9.8%; Score 138.5;
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                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus polypeptide SEQ ID NO 8802.
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                                                                                                                                                                                                                                                                                                                                             ABP29813 standard; Protein; 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                        65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus agalactiae
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(GENO-) INST GENOMIC RES.
                                                                                Local Similarity
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N-PSDB; ABN70444.
                                                   354 AA;
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (C Streptococcus pyagenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antimifiammatory ct the specification. The proteins have antibacterial and antimifiammatory cativity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and catibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. C Nucleic acids encoding (I) are used to detect Streptococcus in a compound binds to biological sample. (I) is used to determine whether a compound binds to composition comprising (I) or a nucleic acid encoding (I), may be used to determine whether a compound binds to consider that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be chromatography, immunoassays, and distinguishing/identifying corrects proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PSRELSESVLTSNVKKQLGTNIAM--NQSGAFIINQNKTDLNAKVSSA--PYAINEIKKV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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-NHAVDRGHLIGYALVG-SLRGFDASTSNPKNIATQAAWANQANSNQSTGQNYYETLVRK
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4.1%; Pred. No. 1.4e-05;
ve 48; Mismatches 118; Indels 6.
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fatches 73; Conservative 4
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US-09-107-522A-5038

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US-09-107-522A-6904

US-09-131-6568-2

US-09-311-6568-2

US-08-33-848C-9

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Query Match 100.0%; Score 1418; DB 4; Length 271; Best Local Similarity 100.0%; Pred. No. 1.3e-142; Matches 271; Conservative 0; Mismatches 0; Indels 0

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181 VTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQ 240
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                                                                                                           121 SYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Addms, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF SEQUENCES: 16
NUMBER OF SEQUENCES: 16
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Pred. No. 2e-140;
0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
                                                                                                                                                                                                                                                                                                                                                              241 SSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
                                                                                                                                                                                                                                                                                                                                                                                              241 SSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REPERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEFONE: (818) 795-4010
TELEFAX: (818) 795-4321
; INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
'PWATH: 272 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-393-889-15

Sequence 15, Application US/08393889

Patent No. 6420152

GENERAL INFORMATION:
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Best Local Similarity 99.6
Matches 269; Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                      SYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNA 180
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                                                                                                                                                                                                                                                                                                                                                                                     181 VTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQ 240
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VTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQ
                                                                                                                                                        61 INEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Beckman Instruments, Inc.
APPLICANT: 2500 Harbor Boulevard
APPLICANT: 2510 Harbor Boulevard
APPLICANT: 2510 Harbor Boulevard
APPLICANT: Fulletton, California 92634
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
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1.3e-142;
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Pred. No. 1.3
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APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: MAY, William H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application PC/TUS9409450 GENERAL INFORMATION:
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REGISTRATION NUMBER: 26,769
REFERENCE/DOCKET NUMBER: 39D-1
TELECOMMUNICATION INFORMATION:
TELEFONE: (818) 795-4000
TELEFOX: (818) 795-4000
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
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STATE: California
COUNTRY: USA
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Best Local Similarity
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183 TGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS 242
    TGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
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                                                                                                                                                                                                                                                                                                                       APPLICANT: Adding, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Balei, Marina
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF SEQUENCES: 16
NUMBER OF SEQUENCES: 16
NUMBER OF SEQUENCES: 16
TITLE OF SEQUENCES: 16
TITLE OF SEQUENCES: 16
TITLE OF SEQUENCES: 16
TITLE OF SEQUENCES: 16
TITLE OF SEQUENCES: 16
TITLE PADRESEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CALLATION NUMBER: US/08/393,889
FILING DATE:
                                                                                                                       243 SDNTINEKVLVYNTANGYTINYHNGTPTQK 272
                                                                                               242 SDNTINEKVLVYNTANGYTINYHNGTPTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                      Sequence 9, Application US/08393889
Patent No. 6420152
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Farber, Michael B.
REGISTRATION UNDHER: 32.612
REFERENCE/DOCKET UNDHER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
TOPOLOGY: ):-
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Matches 229; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
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TGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 YGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNAV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 NEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALA-QTQVSNDVVLNDGASKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYL
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                                                                                                                                                                                                                                                                                                                    Sequence 15, Application PC/TUS9409450
(GENERAL INFORMATION:
APPLICANT: Beckman Instruments, Inc.
APPLICANT: 2500 Harbor Boulevard
APPLICANT: Recombinant DNase B Derived from TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.6%; Score 1397.5; DB 99.6%; Pred. No. 2e-140; tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: May, William H.
REGISTRATION NUMBER: 26,769
REFERENCE/DOCKET NUMBER: 39D-1357 PCT
TELEPHONE: (818) 795-4000
TELEPHONE: (818) 795-4000
TELEPHONE: (818) 795-5321
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      242 SDNTINEKVLVYNTANGYTINYHNGTPTOK 271
                                                                                                                                                                                                             SDNTINEKVLVYNTANGYTINYHNGTPTQK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Beckman Instruments, Inc.
2500 Harbor Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 272 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.6
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein
PCT-US94-09450-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Fullerton
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                        183
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FRAGMENT TYPE: NORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 102
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223 PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
                          181 PIXNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.0%; Score 1220; DB 5; Length 229; 100.0%; Pred. No. 1.2e-121; Live 0; Mismatches 0; Indels (
                                                                                                                                         Sequence 9, Application PC/TUS9409450
GENERAL INFORMATION:
APPLICANT: Beckman Instruments, Inc.
APPLICANT: 2500 Harbor Boulevard
APPLICANT: Fullerton, California 92634
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BE PC compatible
COMPUTER: IB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
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26,769
BR: 39D-1357 PCT
                                                                                                                                                                                                                                                                                                                                          E: Beckman Instruments, Inc. 2500 Harbor Boulevard
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-UUN-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: May, William H.
REGISTRATION NUMBER: 26,769
REFERENCE/DOCKET NUMBER: 391
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (818) 795-621
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100."
Matches 229, Conservative
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                                                                                                                                                                                                                                                                                                                                                                            CITY: Fullerton
STATE: California
COUNTRY: USA
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ORGANISM: Str
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                                                                                                                          PCT-US94-09450-9
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                                                                                                                                                         DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application PC/TUS9409450
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beckman Instruments, Inc.
APPLICANT: 2500 Harbor Boulevard
APPLICANT: Validation By 2634
ITLE OF INVENTION: Recombinant DNase B Derived from TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 43; Conservative 0; Mismatches 0;
Sequence 1, Application US/08393889
Patent No. 6420152
GAPPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derivy
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                             225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELECHIONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Beckman Instruments, Inc. STREET: 2500 Harbor Boulevard CITY: Fullerton STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                        STREFT: 225 South Lake Avenue, CITY: Pasadena STATE: California COUNTRY: USA ZIP: 91001
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (818) , __
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FUNGTH: 43 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
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GENERAL INFORMATION:
APPLICANT: Beckman Instruments, Inc.
APPLICANT: 2500 Harbox Boulevard
APPLICANT: Fullerton, California 92634
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ROTOVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
14.2%; Score 202; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUCTURENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-JUN-1993
ATTORNEY AGENT INFORMATION:
NAME: May, William H.
REGISTRATION NUMBER: 26,769
REFERENCE/DOCKET NUMBER: 39D-1357 PCT
TELECOMMUNICATION INFORMATION:
TELECHIONE: (818) 795-4000
TELEPHONE: (818) 795-4000
TELEPHONE: (818) 795-4000
TELEPHONE: (818) 795-4000
TELEPHONE: (818) 795-4000
TELEPHONE: (818) 795-6121
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Beckman Instruments, Inc. 2500 Harbor Boulevard
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptococcus pyogenes US-08-393-889-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptococcus pyogenes
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 795-6321
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2500 Harbon
CITY: Fullerton
STATE: California
COUNTRY: USA
                                                                                                                                                                                                LENGTH: 38 ammino acid
                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US94-09450-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08393889
Fatent No. 6420152
GENERAL INFORMATION
GARERAL INFORMATION
GARERAL STATE
GARERAL STATE
TILE OF INVENTION: Streptococcus pyogenes
TITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                            COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: Parent in PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
CLLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-AUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: May, William H.
REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 26,769
REFERENCE/DOCKET NUMBER: 26,769
REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 26,769
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REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 26,769
REGISTRATION NUMBER: 39D-1357 PCT.
TELEPHONE: (818) 795-621
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LEMGTH: 43 amino acide
LENGTH: 43 amino acide
TVPE: Amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 91001
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US94-09450-1
       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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PCT-US94-09450-6

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APPLICANT: 2500 Harbor Boulevard
APPLICANT: Fullerton, California 92634
ITILB OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
STREST: 2500 Harbor Boulevard
CITY: Fullerton
CITY: Fullerton
STRATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 32;
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; Patent No. 6280993
; GENERAL INFORMATION:
APPLICANT: YAMATO, Ichiro
APPLICANT: HOSAKA, Toshiaki
TITLE OF INVENTION: GENE ENCODING CLASS I COLLAGENASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burgess, Ryan and Wayne
STREET: 370 Lexington Avenue, Suite 2105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/09450

FILING DATE: 18-AUG-1994

CLASSIPICATION NUMBER: US 08/082,845

FILING APPLICATION DATA:

APPLICATION NUMBER: US 08/082,845

FILING BATE: 23-JUN-1993

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 39D-1357 PCT

TELECOMMUNICATION NUMBER: 39D-1357 PCT

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: 39D-1357 PCT

TELECOMMUNICATION NUMBER: 39D-1357 PCT

TELECOMMUNICATION NUMBER: 39D-1357 PCT

TELEROMMUNICATION NUMBER: 39D-1357 PCT

TELEROMMUNICATION NUMBER: 39D-1357 PCT

TELEROMMUNICATION NUMBER: 39D-1357 PCT

TELEROMMUNICATION NUMBER: 39D-1357 PCT

TELEROMMUNICATION NUMBER: 39D-1357 PCT

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TELEROMMUNICATION NUMBER: 30D-1357 PCT

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TELEROMMUNICATION NUMBER: 30D-1357 PCT

TELEROMMUNICATION NUMBER: 30D-1357 PCT

TELEROMMUNICATION NUMBER: 30D-1357 PCT

TELEROMMUN
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Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 QTQVSNDVVLNDGASKYLNEALAWTFNDSPNY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QTQVSNDVVLNDGASKYLNBALAWTFNDSPNY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10017
TANARIE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch disk
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM; WINDOWS 98
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Flappy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-BDDWW-RR: Patenty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOLECULE TYPE: peptide HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US94-09450-16
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0
                                                                                                                                                                 Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/08393889
Fatent No. 6420152
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: EM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PETENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/393,889

FLING DATE:

CLASSIFICATION NUMBER: US/08/393,889

FLING DATE:

APPLICATION NUMBER: US/08/393,889

FLING BATE:

MAMB: FSPLICATION NUMBER: US/08/082,845

FILING BATE:

MAMB: FSPLICATION NUMBER: US/08/082,845

FILING BATE:

TELEPHONE: (818) 796-4000

TELEPHONE: (818) 796-4000

TELEPHONE: (818) 796-4000

TELEPHONE: (818) 796-4000

TELEPHONE: (818) 796-4000

TELEPHONE: CHARACTERISTICS:

LENGTH: 32 amino acids

LYPR: Amino acids

TYPR: Amino acids
                                                                                                                                                                                                                                                                           43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 80
                                                                                                                                                                                                                                                                                                                    - 1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 38
                                                                                                                                         Query Match

14.2%; Score 202; DB 5; I
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 QIQVSNDVVLNDGASKYLNEALAWTFNDSPNY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QTQVSNDVVLNDGASKYLNEALAWTFNDSPNY 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application PC/TUS9409450 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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APPLICANT: Beckman Instruments, Inc.

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Gaps

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179 NAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.0%; Score 113; DB 4; Length 97; Best Local Similarity 32.3%; Pred. No. 0.00018; Matches 30; Conservative 14; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 MOS-SDNTINEKVLVYNTANGYTINYHNGTPTQ 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sheldon & Mak
STRET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 AESIEDKKIEFNVFIYNVQDGYTINYETGQATK 94
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007
TELEPAX: (781)893-507
INFORMATION FOR SEQ ID NO: 5038:
SEQUENCE CHARACTERISTICS:
                          APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...97
SEQUENCE DESCRIPTION: SEQ ID NO: 5038:
                                          FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2,1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08393889 Patent No. 6420152
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 97 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-107-532A-5038
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US-08-393-889-4
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Sequence 5038, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 ------ANTNSEKYDFEYLNGLSYTELTNLIKNIKWNQINGLFNYST 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 G-----GDALRVNAVTGTRTQNVGGR-----DQKGGMRYTE-QRAQEWLEANRDGYLYYE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 GSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYV-----GDFWNR-SHLIADSL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 GSQKFFGDKNRVQAIINALQES--GRTYTANDMKGIETFTEVLRAGFYLGYYNDGLSYLN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 VAPIYNADELIPRAVVVSMQSSDN----TINEKV-----LVYN-TANGYTINYHNGTP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 DRNF--QDKCIP--AMIAIQKNPNFKLGTAVQDEVITSLGKLIGNASANAEVVN--NCVP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NDGASK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.1%; Score 114.5; DB 3; Length 1118; Best Local Similarity 22.8%; Pred. No. 0.0055; Matches 69; Conservative 45; Mismatches 100; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 FSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
US/09/379,523
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                                     CLASSIFICATION: 435
CLASSIFICATION ATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 17,906
REFERENCE/DOCKET NUMBER: U-Wp-
TELECPHONE: 212-639-8150
TELEPHONE: 212-639-8150
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COUNTRY: USA
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide US-09-379-523-3
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Waltham
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7.5%; Score 106; DB 4; Length 23;
Best Local Similarity 95.7%; Pred. No. 0.00011;
Matches 22; Conservative 0; Mismatches 1; Indels
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPRONE: (818) 795-4000
TELEPRONE: (818) 795-4001
TELEPRONE: (818) 795-5321
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid TYPE: amino acid TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ONGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
US-08-393-889-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 QTQVSNDVVLNDGASKYLNEALA 66
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Search completed: January 5, 2004, 18:44:01 Job time : 32.9429 secs

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APPLICALLES
FILING DATE:
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: RAIDEN, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECHONIALCATION INFORMATION:
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TELECHONIALCATION INFORMATION:
TELECHONIALCATION INFORMATION:
TELECHONIALCATION INFORMATION:
TELECHONIALCATION INFORMATION:
TELECHONIALCATION INFORMATION:
TELECHONIALCATION INFORMATION:
INFORMATION FOR SEQ ID NO: 8:
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Sequence 15, Appli
Sequence 1, Appli
Sequence 16, Appli
Sequence 16, Appl
Sequence 129, Appl
Sequence 7751, Appli
Sequence 412, Appli
Sequence 412, Appli
Sequence 1751, Appli
Sequence 212, Appli
Sequence 212, Appli
Sequence 212, Appli
Sequence 212, Appli
Sequence 2, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                        January 5, 2004, 18:41:44; Search time 502.074 Seconds (without alignments) 108.298 Million cell updates/sec
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                                                                                                                                                                                                                                                                     1418
1 MNLLGSRRVFSKKCRLVKFS......VYNTANGYTINYHNGTPTQK 271
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB_pep:*
3: /cgn2_6/ptodata/2/pubpaa/NEM_PUB_PEP:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_DEP:*
5: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_DEP:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_DEP:*
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13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-172-502-17
US-10-124-880-2
US-10-156-761-14080
US-10-441-626-3
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US-09-119-900-15
US-09-119-900-1
US-09-119-900-1
US-09-119-900-16
US-09-119-900-16
US-09-769-736-129
S US-09-769-74A-168
S US-09-769-74A-168
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                                                                                                                                                                                                                                                                                                                                                                                                                          733937 segs, 200641211 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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1397.5
1220
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126.5
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Sequence 314, App Sequence 7834, App Sequence 1039, App Sequence 1039, App Sequence 1039, App Sequence 1039, App Sequence 20377, App Sequence 20377, App Sequence 1312, App Sequence 128147, App Sequence 128147, App Sequence 128147, App Sequence 128147, App Sequence 128147, App Sequence 128147, App Sequence 128147, App Sequence 128147, App Sequence 128147, App Sequence 128147, App Sequence 128147, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2, App Sequence 2,
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                                            Sequence 3,
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| Patent No. US20020081622A1
| GENERAL INFORMATION |
| APPLICANT: Addms, Craig W. APPLICANT: Belei, Marina |
| TILE OF INVENTION | Streptococcus pyogenes |
| TILE OF INVENTION | Streptococcus pyogenes |
| NUMBER OF SEQUENCES: 16 |
| CORRESPONDENCE | Sheldon & Mak |
| STREET: 225 South Lake Avenue, Ninth Floor
4 US-10-075-872-3

5 US-10-261-997-3

US-09-9397-3

US-08-9493-354

5 US-10-369-493-354

5 US-10-369-493-21495

2 US-10-336-9493-1039

2 US-10-336-9493-1039

2 US-10-369-493-1039

2 US-10-284-000-8

2 US-10-369-493-1312

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparishe
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-369-493-21586
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: USA
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STATE: Californi
COUNTRY: USA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 952
TELECOMMUNICATION INFORMATION
TELEPHONE: (818) 796-4000
                                                                           Query Match
Best Local Similarity 99.6%;
Matches 269; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID No. 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 229 amino acids
amino acid
             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-119-900-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Par
STATE: Ca
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                                                                                                                                                                                                                                                                61 LINEALAWTENDSPINYXKTLGTSQITPALFPKAGDILYSKLDELGRIRTARGTLITYANVEG 120
                                                                                                                                                                                                                                                                                                         121 SYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNA 180
                                                                                                                                                                                                                                                                                                                                 VIGIRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQ 240
                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY
                                                                                                                                                       0; Gaps
                                                                                                                        Length 271;
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09119900
Patent No. US20020081622A1
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from VNMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                              100.0%; Score 1418; DB 9;
100.0%; Pred. No. 9.9e-137;
:ive 0; Mismatches 0;
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COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                         SSDNTINEKVLVYNTANGYTINYHNGTPTOK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 SSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
ATTORNEY/AGENT INFORMATION:
NAME: FRIDER, MICHAEL B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                 : 271 amino acids
amino acid
3Y: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS: LENGTH: 272 amin.
                                                                                                          Query Match
Best Local Similarity 100.
Matches 271; Conservative
SEQUENCE CHARACTERISTICS LENGTH: 271 amino acic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 amino acids amino acids
                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-119-900-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-119-900-15
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62 NEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGS 121
                                                                                                                                                                                                                                122 YGVRQSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNAV 181
                                                                                                                                                                                                                                                              2 NILGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYL
                                                                                                                                                                                                                                                                                                              182 IGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS
                                              Gaps
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Score 1397.5; DB 9; Length 272;
Pred. No. 1.3e-134;
0; Mismatches 0; Indels 1;
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Folosomolos SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: BPLICATION NUMBER: US/09/119,900 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09119900
Fatent No. US2002001622A1
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Adams, P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                         242 SDNTINEKVLVYNTANGYTINYHNGTPTQK 271
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Gaps ; 0

Length 43;

us-08-482-785-8.rapb

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1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR
                                                                                              1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR
                Query Match 14.3%; Score 203; DB 9; L
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 43; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
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Best Local Similarity
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CITY: Pasadena
STATE: Californi
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HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 91001
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                       43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 102
                                                                                                                                                                                                                                     103 LGRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 162
                                                                                                                                                                                                                                                                                                                                         121 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 180
                                                                                                                                                                                                                                                                                                                   163 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 222
                                                                                                                                                                              1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 60
                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     223 PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
                                                                           Length 229;
                                                                                                                  0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                           Score 1220; DB 9; 1
Pred. No. 1.5e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09119900
| Patent No. US20020081622A1
| GENERAL INFORMATION:
| APPLICANT: Pang, Patty P.-Y.
| APPLICANT: Pang, Patty P.-Y.
| APPLICANT: Pang, Recombinant DNase B Deriv:
| TITLE OF INVENTION: Streptococcus pyogenes
| NUMBER OF SEQUENCES: 16
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Sheldon & Mak
                                                             86.0%; Scor.
100.0%; Pred. No. 100.0%; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                      Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Streptococcus pyogenes
US-09-119-900-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 955
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-terminal
                                                                       Query Match
Best Local Similarity 100.0
Matches 229; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Pasadena
STATE: California
COUNTRY: USA
ZIP: 91001
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ORIGINAL SOURCE
                ) ORGANISM:
US-09-119-900-9
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Sequence 6, Application US/09119900
Patent No. US20020081622A1
GENERAL INFORMATION:
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 202; DB 9; L
100.0%; Pred. No. 1.7e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                      E: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DAIE:
CLASSIFICATION:
PRIOR APPLICATION UNBER: US/08/082,845
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEFAX: (818) 795-6321
TELEFAX: (818) 795-6321
; INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
; **CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-119-900-16; Sequence 16, Application US/09119900; Patent No. US20020081622A1; GENERAL INFORMATION:
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us-08-482-785-8.rapb

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131 NONPAGW--TGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGD-----ALRVNA 180
                                                                                                                                                                                                                          181 VTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNAD-ELIPRAVVVSM 239
                                                                                                                                                                                                                                                                                                                  72 SPNYYKTLGTSQITPALFPKAGDILYSKLDE--LGRTRTARGTLTYANVEGSYGVRQSFG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 KNQNPAGWIGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSL----GGDALR---VNAV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 TGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQ 240
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                                                                                                                                                           26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 ADNKTKTVGKETV-----PTVANALLSKATRQYKNRKETGNGSTSW-------
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                                                                                                          9.2%; Score 131; DB 12; Length 261; 26.0%; Pred. No. 5.6e-05; tive 25; Mismatches 60; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

8.9%; Score 126.5; DB 12; Length
Best Local Similarity 21.9%; Pred. No. 0.00017;
Matches 59; Conservative 37; Mismatches 108; Indels
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JENDERAL INCUCRALIUN;
JAPPLICANT: Le Page, Richard WF
APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Gean B
APPLICANT: Hanniffy, Gean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21122WO
CURRENT APPLICATION NUMBER: US/09/769,744A
CURRENT FILING DATE: 1999-07-27
PRIOR PILING DATE: 1999-07-27
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PATENT NOS: 196
SOFTWARE: PATENT NOS: 196
SOFTWARE: PATENT NOS: 196
SOFTWARE: PATENT NOS: 196
SOFTWARE: PATENT NOS: 196
SEQ ID NO 168
                                                                                                                                                                                                                                                                                                                                                                        240 OSSDNTINEKVLVYNTANGYTINYHNGTPT 269
                                                                                                                                                                                                                                                                                                                                                                                                                230 KSQDGTLEFNVAIPNTQASYTMDYATGEIT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 168, Application US/09769744A Publication No. US20030134407A1 GENERAL INFORMATION:
                                       ; ORGANISM: Streptococcus agalactiae US-09-769-736-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-744A-168
                                                                                                                                                    39; Conservative
                                                                                                                             Best Local Similarity
Matches 39; Conserv
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                  TYPE: PRT
                                                                                                        Query Match
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12.0%; Score 170; DB 9; Length 32
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 32; Conservative 0; Mismatches 0; Indels
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                       E: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 QTQVSNDVVLNDGASKYLNBALAWTFNDSPNY 75
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Publication No. US2003013875A1
SEMERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Mells, Jeremy M
APPLICANT: Wells, Jeremy M
APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILIE REPERENCE: PWC/P21089w0
CURRENT FILING DATE: 2003-02-14
PRIOR PELING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125163
PRIOR PELING DATE: 1998-07-27
PRIOR PELING DATE: 1998-07-31
PRIOR FILING DATE: 1998-07-31
PRIOR PELING DATE: 1998-07-31
SOFTWARE: PARENT NOWER: 1998-07-31
SOFTWARE: PARENT NOWER: 1998-07-31
SOFTWARE: PARENT NOWER: 1998-03-19
SOFTWARE: PARENT NOWER: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 796-4100
INFORMATION: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              3: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                     STATE: California
COUNTRY: USA
ZIP: 91001
                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                    ADDRESSEE: Shel
STREET: 225 Sou
CITY: Pasadena
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US-09-119-900-16
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LENGTH:

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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                       APPLICATION NUMBER: US/09/119,900
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Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 OTQVSNDVVLNDGASKYLNEALA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 OTOVSNOVVLNDGASXYLNEALA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.59
Best Local Similarity 22.89
Matches 55; Conservative
                                             CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-738-626-4312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 FASRLRLVKLPACALQTPEAEGCTDREFVPVDNDTATGTLTATVTA-AADTEVS---- 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 DGAS-KYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELG--RTRTARG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 -GASTQLMREASA---SGASVYTLASGSSS-----DAGDYRASTLSPTGSWEVSTGSG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 AFTYNVPIQLPKPPMGSAPSLSLSYNSQSVDGRTSASNNQASWAGMGWDLNVGYIERRYR 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---RSHLIADSLGGDALRVNAVTGTRT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 NCSEDGLPTIGDMCWDSPNSAKEPSGAVYVINLNGVTSELIQDNTGSGAYHLKNDPGWRV 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 FSKKCRLVKFSMVAL------VSATMAVTTVTLENTALARQTQVSNDVVLN
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APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABRESS:
ADBRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
ZIP: 91001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 QNV----GGRDQKGGMRYTEQRAQEWLEANRDGYLYY 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            469 ORLFDGYGAGRD-----GEYWVISTODGORYY 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.7%; Score 109.5; DE 24.1%; Pred. No. 0.23; tive 28; Mismatches
                                                                                                            APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, JUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 15109
                                          Sequence 7751, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Streptomyces avermitilis US-10-156-761-7751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09119900
Patent No. US20020081622A1
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 24.1<sup>1</sup>
Matches 67; Conservative
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APPLICANT: TATEISHI, NACKO
APPLICANT: TATEISHI, NACKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CLASSIFICATION:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFREENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEFONE: (818) 795-631
TELEFONE: (818) 795-631
JINFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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CURRENT FILING DATE: 2000-12-18
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PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1990-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PELING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
LENGTH: 1233
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RESULT 14
US-10-156-761-14080
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                       1182 EVIRPIAQINYSRHDWANAARLIPRLTGFDLVSAE----AKVL-----SAINNNIIP 1230
                                                                                                           1072 RNSGLEAMRNGLGADQFSÅEFISADSRLRAQLEWLENRRELNDLGQLPTLFDFAEKYEYL 1131
                                                                       119 --EGSYGVROSFGKNONPAGWTGNPNHVKYKIEWLNG-----LSYVGDFWNRSHLI 167
                                                                                                                                                 168 ADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLY-----Y 219
YLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANV- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 TLGTSQITPALFPKAGDI-LYSKLDE-----LGRIRTARGTLTYA--NVEGSYGVRQSF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 ------GKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 FSRFTVIN-TMAAPTTTSTTT---SILTSNSVVNKDNFNEHMN-----LSGSATYDP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VIGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TPRSDA 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/10172502
Publication No. US20030185933A1
GENERAL INFORMATION.
APPLICANT: FOSTER, Timothy et al.
APPLICANT: FOSTER, Timothy et al.
TILLE OF INVENTION: CROSS-REACTIVE MONOCLONAL AND POLYCLONAL ANTIBODIES.
FILE REPERENCE: P072631031/BAS
CURRENT APPLICATION NUMBER: US/10/172,502
CURRENT APPLICATION NUMBER: US/10/172,502
PRIOR APPLICATION NUMBER: US/10/172,502
PRIOR APPLICATION NUMBER: US/10/172,502
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
ERNGTH: 522
                                                                                                                                                                                     1132 IDHLGDDRIK---VTARELSTLASEHRRG-----NAENWLYAPYVSFIYSLLNRMIAH
                                                                                                                                                                                                                           220 EV-API----YNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.9%; Score 98; DB 12; Length 522; Best Local Similarity 21.4%; Pred. No. 0.37; Matches 58; Conservative 39; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 SPGPLGQIGKEGAAVGIGGLNNAFGFKLDTYHNTS----
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US-10-172-502-17
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Sequence 2, Application US/10124880 Publication No. US20030026810A1 GENERAL INFORMATION: APPLICANT: Jorgensen, Per Lina

US-10-124-880-2

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APPLICANT: Andersen, Lene No. US20030026810Alboe
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
TITLE OF INVENTION: No. US20030026810Alel Rhamnogalacturonan Hydrolases
FILE REFERENCE: 5572 204 US
CURRENT APPLICATION NUMBER: US/09/311,626B
PRIOR APPLICATION NUMBER: US/09/311,626B
PRIOR APPLICATION NUMBER: 060898
PRIOR PILING DATE: 1998-05-01
PRIOR PILING DATE: 1998-05-01
PRIOR PILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 61
SOFTHARE: PastSEQ for Windows Version 4.0
SOFTHARE: PastSEQ for Windows Version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 EGSYGVRQSFGKNONPAG-----WTGN------PNHVKYKIEWLNGLSYVGD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 NEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILY---SKLDELGRTRTARGTLTYANV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F-----WNRSHLIADSLGG-----DALRVNAVTGTRTQNVG-GRDQKGGMRY 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 TEQRAQEWLEANRDGYLYYEVAPIYNAD----ELIPRAVVVSMQSSDNTINEKVLVYNTAN 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 VFSKKCRLVKFSMVALVSATMAVTTVTLE-NTALARQTQVSN-----DVVLNDGASKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MFSKRLHHFWRVMLGLVVVVSTIGSVFLPVSTASAAPROAENISRGLVAVKVSSGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOS-10-126-761-14080

J. Sequence 14080, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:
J. APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATTORI, WOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRENENE: 29-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PELING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PLING DATE: 2001-06-30
PRIOR PLING DATE: 2001-06-30
PRIOR PLING DATE: 2001-06-30
PRIOR PLING DATE: 2001-06-30
PRIOR PLING DATE: 2001-06-30
PRIOR PLING DATE: 2001-06-30
PRIOR PLING DATE: 2001-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 94; I 21.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bacillus sp. AA 386
US-10-124-880-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 21.08
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYVLS 262
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Query Match 6.5%; Score 92; DB 12; Length 234;
Best Local Similarity 23.7%; Pred. No. 0.47;
Matches 70; Conservative 24; Mismatches 77; Indels 124; Gaps 17;
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                                                                                                                                                                                                                                                                                                                                                           124 VRQSFGKNONP-----AGWIGNPNHVKY-----KIEWLNGLSYVGDFWN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 VRNSLAELTSARTTLKODATIPGTSWATDPETNKVVVTADRTVSKAEWATLTKVVDGLGQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 RSHL-----IADSLGGDALRVNAVIGIRIQNVGGRDQ-----KGGMRY---- 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 RAELORTKGEYKPFIA---GGD----AITGG-----GGRCSLGFNVVKGGOPYFITAGH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TEQ-----ELIPRAVIVSMQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 CTESISTWSDSSGSQIGTNEQSSFPGNDFGLVKY----TSNADHPSEVDLYNGSTQPITK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YLNEALAWTFNDSPNYYKTLGTSQI------TPALFPKAGDILYSKLDELGRTRTAR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 HAD-----WQWSGGQNNVKSYQNSQIAIPQKRTVNSISSMPTTASWSYS------ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 GTLTYANVEGSYGVRQSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDF----WNRSHL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 IADSLG--GDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|| | ||: | :| ||:
| MKFLQVLPALIPALIAQTSCDQWATFTGNGYTVSNNLWGASAGSGFGCVTAVSLSGGASW 60
                                                                                                                                                                                                                       4 LGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAROTQVSNDVVLNDGASKYLNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 VKFSMV--ALVSATMAVTTVTLENTALARQTQVSND-------VVLNDGASK 59
                                                                                                                                                                                                                                                         29 LKHRRISRRRAAVAGAGIAALVAAGVTFQTA---NASEAPKTEAPHTLSLS-AAGK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10441626
Publication No. US2030186418A1
GENERAL INFORMATION:
APPLICANT: Gualfetti, Peter
APPLICANT: Mitchinson, Colin
APPLICANT: Mitchinson, Colin
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
FILE REPERENCE GG31
CURRENT APPLICATION NO. US2030196418A1e1 Variant EGIII-Like Cellulase
CURRENT APPLICATION NO. US2030196418A1e1
TITLE OF INVENTION: Compositions
FILE REPERENCE GG31
CURRENT FILING DATE: 2003-05-19
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 3
                                                                                                                                                                            Gaps
                                                                                                                 Query Match 6.5%; Score 92.5; DB 15; Length 388; Best Local Similarity 23.7%; Pred. No. 0.88; Matches 78; Conservative 32; Mismatches 114; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SSDNTINEKVLVYNTANGYTINYHNGTPT 269
                                              ORGANISM: Streptomyces avermitilis US-10-156-761-14080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Trichoderma reesei
LENGTH: 388
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5.1.6	Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 5, 2004, 17:31:14; Search time 31.442 Seconds (without alignments) 828.882 Million cell updates/sec

Title: Perfect score: Sequence:

US-08-482-785-8 1418 1 MNLLGSRRVFSKKCRLVKFS......VYNTANGYTINYHNGTPTQK 271

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76: * 1: pir1: * 2: pir2: * 3: pir3: * 4: pir4: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mitogenic factor,	deoxyribonuclease	hypothetical prote	υ	endA protein - Str	deoxyribonuclease	probable outer mem	streptogrisin D (E	hypothetical prote	uncharaterized con	conserved hypothet	alpha-toxin precur	probable fimbrial	flagellin - Escher	endo-arabinase rel	pullulanase - Ther	P-glycoprotein - T	flagellar hook pro	hypothetical prote	Alpha-Hemolysin pr	pro		conserved hypothet	botulinum neurotox	hypothetical prote	conserved hypothet	hemolysin accessor	hypothetical prote	
SUMMARIES	ID	836907	JT0584	D86644	F95229	S10641	A99094	G71896	A56123	E84483	F97223	AB1481	S69209	E83521	B48658	H96970	S27545	T30295	E70460	E84280	F89887	876211	C56617	D69957	S58857	S76412	AG1120	T31104	AH2060	JC5558
	DB	7	~	0	~	~	N	~	~	~	~	~	~	~	7	7	7	7	~	~	7	~	N	7	~	~	7	~	7	7
	Length	271	327	263	274	274	274	455	392	928	347	386	319	839	595	9/9	1203	1534	8	363	319	611	869	638	292	4199	386	474	743	396
* Ouerv	Match	99.7	27.2	10.8	8.9	8.9	8.9	•		7.1	6.9		٠	6.7		•	9.9	9.9	6.5	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.3	6.3	6.3	6.3
	Score	1414	385	153.5	126.5	126.5	126.5	104.5	104	100	98.5	96.5	95.5	95.5	σ	93.5	93	93	92.5	92	91.5	91.5	91.5	16		90.5	90	90	89.5	83
Regult	SO.	н	7	ო	4	ស	9	7	8	đ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25		27	28	29

proteinase (import	cobalamin biosynth	periplasmic mannit	mevalonate kinase	outer membrane pro	outer membrane pro	prolyl oligopeptid	oligopeptidase B (autolysin (amidase	penicillin amidase	scaffolding protei	cellulase (EC 3.2.	hypothetical prote	outer membrane por	glutamate dehydrog	probable glutamate
AI1930	D64413	AE3449	F64435	D90755	B85619	H95155	C98022	AG1565	139665	T30433	S29043	F83068	MMECF	JN0854	A71038
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488	1232	255	312	362	362	646	646	774	802	1162	941	2154	362	420	422
6.3	6.3	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.1	6.1	6.1
89	89	88.5	88.5	88	88	88	88	88	88	88	87.5	87.5	87	87	87
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT	1
mitogenic	nic factor, 25K, precursor - Streptococcus pyogenes
C;Speci C;Date:	C;Species: Streptococcus pyogenes C;Date: 10-Dec-1993 #sequence revision 23-Feb-1996 #text change 15-Oct-1999
C, Acces	saion: 836907; 836908; \$29188
K; IWABA	K;Iwasaki, M.; igarasni, H.; Hinuma, I.; Incendo, I. FEBS Lett. 331, 187-192, 1993
A;Title A:Refer	A;Title: Cloning, characterization and overexpression of a Streptococcus pyogenes gene e A;Reference number: 836907; MUID:94009636; PMID:8405402
A, Acces	
A;Molecule A;Residues:	
A; Cross	A;Cross-references: EMBL:D13428; NID:g432369; PIDN:BAA02693.1; PID:d1003198; PID:g432370
A, Molecule	wule type: protein
A; Residues R; Yutsudo,	A;Kesiques: 44-64 <iww> R;Yutsudo, T.; Murai, H.; Gonzalez, J.; Takao, T.; Shimonishi, Y.; Takeda, Y.; Igarashi,</iww>
FEBS Le	
A;Title A;Refer	A;Title: A new type of mitogenic factor produced by Streptococcus pyogenes. A;Reference number: S29188; MUID:92354761; PMID:1644200
A; Acces	A;Accession: S29188
A, Resid	
F;1-43/ F;44-27	F;1-43/Domain: signal sequence #status predicted <sig> F;44-271/Product: mitogenic factor, 25K #status experimental <mat></mat></sig>
Query	99.7%; Score 1414
Best Loc Matches	Best Local Similarity 99.6%; Pred. No. 9.98-111; Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
ò	1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY 60
. q a	1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY 60
ò	61 INBALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDBLGRIKTARGARGTLTYANVEG 120
qq	61 LNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEG 120
ò	121 SYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNA 180
qq	121 SYGVRQSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNA 180
ò	181 VTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQ 240
qq	181 VTGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEAAPIYNADELIPRAVVVSMQ 240
ò	241 SSDWINEKVLVYNTANGYTINYHNGTPTQK 271
qq	241 SSDNTINEKVLVYNTANGYTINYHNGTPTQK 271

98

261

us-08-482-785-8.rpr

```
C;Species Streptococcus pneumoniae (strain TIGR4)
C;Species Streptococcus pneumoniae
C;Bate: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: F95229
C;Accession: F95229
C;Accession: F95229
C;Accession: F95229
C;Accession: F95229
C;Accession: F95229
C;Accession: F95229
C;Accession: F95229
A;Athckey, E.K.; Holt, E.
Scalzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.
Scalcace 293, 498-696, 2001
A;Title: Complete Genome Sequence of a virulent isolater, J.C.; Dougherty, B.A.; Morrison, A;Reference number. A95000; MUID:21357209; PMID:11463916
A;Scatus: preliminary
A;Residiner 1-2.
A;Residiner 1-2.
A;Residiner 1-2.
A;Residiner 1-2.
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                                                                                                                                          SPNYYKTLGTSQITPALFPKAGDILYSKLDE--LGRTRTARGTLTYANVEGSYGVRQSFG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 KNONPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSL----GGDALR---VNAV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 IGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 VQTAWANQAQAEYSTGQNYYESKVRKALDQNK--RVRYRVTLYYASNEDLVPSASQIEAK 242
                                                39 İDNSSQVSTKSLASSVKQAPLTFKNQRQMVMANTDALGRAVDSHIQLKDSQEPKVKREPL
                                                                                                     TYANVEGSYGVRQSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDFW--NRSHLIA---
                                                                                                                                                                                                     169 DSLGGDALRV-----NAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYY
                                                                                                                                                                                                                                                  SGLNNEARNLVPETAWFIGGNFTGTNDGNT-----ASMLYYENRLDSWLANHPNYYLDY
                                                                                                                                                                                                                                                                                                        EVAPIYNADELIPRAV---VVSMQSSDNTINEK-------VLVYNTANGYTI
                                                                                                                                                                                                                                                                                                                                     37 TNLSQKKQASEAPSQALAESVLTDAVKSQIKGSLEWNGSGAFIVNGNKTNLDAKVSSKPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.9%; Score 126.5; DB 2; Length 274; 21.9%; Pred. No. 0.0044; Live 37; Mismatches 108; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 TFNDSPNYYKTLGTS-QITPALFPKAGDILYSKLDELGRT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 TTVTLENTALAROTQVSNDVVLNDGASKYLNEALAWTFND-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 SSDNTINEKVLVYNTANGYTINYHNGTPT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 SSDGELEFNVLVPNVQKGLQLDYRTGEVT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
S10641
endA protein - Streptococcus pneumoniae
C,Species: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 21.99
Matches 59, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          262 NYHNGT 267
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A,Gene: SP1964
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                                             Dypothetical protein ypfB (imported) - Lactococcus lactis subsp. lactis (strain IL1403) (Species Lactococcus lactis subsp. lactis (Species Lactococcus lactis subsp. lactis (Species Lactococcus lactis subsp. lactis (Species Lactococcus lactis subsp. lactis (Species Lactococcus lactis subsp. lactis (Species Lactococcus lactis subsp. lactis Lactococcus lactis Lactococcus lactis Lactococcus Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus lactis Lactococcus Lactococcus lactis Lactococcus Lactococcus lactis Lactococcus Lactococcus lactis Lactococcus Lactococcus lactis Lactococcus Lactococcus lactis Lactococcus Lactococcus lactis Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococcus Lactococc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 RAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLYYNTANGYTINY 263
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deoxyribonuclease I (EC 3.1.21.1) sdc precursor - Streptococcus "equisimilis"
N'Alternate names: streptodornase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 SKKCR--LVKFSMVALVS-ATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALAW 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.2%; Score 385; DB 2; Length 327; Best Local Similarity 33.0%; Pred. No. 1.4e-24; Matches 100; Conservative 39; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                             A;Gene: sdc
C;Keywords: hydrolase
C;Keywords: hydrolase
F;1-35/Domain: signal sequence #status predicted <NIG>
F;36-308/Product: deoxyribonuclease sdc #status predicted <MAT>
-- ^ ^ ^ ^ Anne 385; DB 2; Length 327
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10.8%; Score 153.5; DB 2;
Best Local Similarity 24.4%; Pred. No. 2.3e-05;
Matches 60; Conservative 26; Mismatches 85;
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R,Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Tves, C.; Gibbon, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE001503; GB:AE001439; NID:g4155275; PIDN:AAD06302.1; PID:g415528
A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accession: A56123
R,Sidhu, S.S.; Kalmar, G.B.; Willis, L.G.; Borgford, T.J.
Biol. Chem. 270, 7594-7600, 1995
A,Title: Protease evolution in Streptomyces griseus. Discovery of a novel dimeric enzyme A,Reference number: A56123; MUID:95221424; PMID:7706307
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C;Species: Streptomyces griseus
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 16-Aug-2002
                                                                                  TGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 DSNPKFKGLGLRAQTTINVIFPVYAKDLYDVYWRNSKIGEWGASLLIHQRFDYNEFNFGF 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNAVT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 GYYONFGNANARIGWYGNPIPFNYR----NNSVYGGVFSN------AITADAVS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTRIONVGGRDOKGGM-----RYT-EORAOEWLEANRDGYLYYEVAPIYNADELIPRAVV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                    probable outer membrane protein - Helicobacter pylori (strain J99)
C,Species: Helicobacter pylori
A,Variety: strain J99
C,Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 DSPNYYKTLGTSQITP--ALFPKAGDILY-----SKLDELGRTRTARGTLTYANVEGSY
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7.4%; Score 104.5; D
Best Local Similarity 25.2%; Pred. No. 0.6;
Matches 53; Conservative 19; Mismatches
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                                                                                                                                                                                                                                                               SSDGELEFNVLVPNVQKGLQLDYRTGEVT 271
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A;Start codon: GTG
C;Superfamily: streptogrisin A
C;Keywords: hydrolase; serine proteinase
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A;Molecule type: DNA
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C,Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Oct-1999
C,Accession: 810641
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deoxyrlbonuclease I (EC 3.1.30.-) [imported] - Streptococcus pneumoniae (strain R6)

clasteis 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001

C.Accession: A99094

R. H. LeBlanc, J.A. Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E R. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; W, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A.Authors: Vang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A; Reference number: A97072; WUID:21429245; PMID:11544234

A; Status: Preliminary

A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 TGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-274 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAL00582.1; PID:g15459463; GSPDB:GN00174
C;Genetics:
A;Gene: endA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 SPNYYKTLGTSQITPALFPKAGDILYSKLDE--LGRTRTARGTLTYANVEGSYGVROSFG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :: : | : | : | | : | This orkoaseapsoalaesvlidavksoikgslewngsgafivngnktnlidakvsskpy 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 INLSQKKQASEAPSQALAESVLIDAVKSQIKGSLEWNGSGAFIVNGNKTNLDAKVSSKPY 96
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8.9%; Score 126.5; DB 2; Length
Best Local Similarity 21.9%; Pred. No. 0.0044;
Matches 59; Conservative 37; Mismatches 108; Indels
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6.8%; Score 96.5;
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Matches 65; Conserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein At2g07240 [imported] - Arabidopsis thaliana (S.Species: Arabidopsis thaliana (mouse-ear cress) (S.Species: Arabidopsis thaliana (mouse-ear cress) (S.Species: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 16-Feb-2001 F.Libarion (S. Parcession: E84483 F.Libarion (S. P. Fallon, E. P. P. Penito, M. I. Town, C.D.; Fujii, C.Y.; Fallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Mature 402, 761-768, 1999 Mite, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A; Title: Sequence and analysis of Chromosome 2 of the plant Arabidopsis thaliana.

A; Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                16;
                                                                                                                               51 VVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGD---ILYSKLDELGRTR 107
                                                                                                                                                   108 TARGTLT-YANVEGSYGVROSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHL 166
                                                                                                                                                                                                                 248
                                                                                                                                                                                                                                                                                                                                                243 TSWSDTQGGSEIGANBGSSFPENDYGLVKYTSDTAHPSEVNLYDGSTQAITQAGDATVGQ 302
                                                                               20
                                                                                              LKHRRISRKRATLAGSAVVALVAAGFTFQTANASDDVPAFGAKTLSADAAGKLATTLDRD 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 PATCMRR---KNHGPIGEKGESSGGVY----FDALSRNIDEKLKAQSEKILKGVIHWFTE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-928 <STO>
A;Cross-references: GB:AE002093; NID:g4309748; PIDN:AAD15517.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SLGGDALRVNAVTGTRTQNVGGRDQKGGMRYT 201
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                                                                                                                                                                                                                                                                                    --NRDGYLYYEVAPIYNAD-ELIPRAVVVSMQSSDNTINE
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                                              Gaps
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                                              88;
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A.Map position: 2
C.Superfamily: Arabidopsis thaliana hypothetical protein T21C14.40
            Length 392;
     7.3%; Score 104; DB 2; Length 392, 22.4%; Pred. No. 0.54;
iive 38; Mismatches 123; Indels
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Best Local Similarity 19.8%; Pred. No. 3.7;
Matches 59; Conservative 47; Mismatches 106; Indels
                                                                                                                                                                                                                                                            167 IADSLGGDALRVNAVTGTRTQNVGGRDQ~-----
                                                               4 LGSRRVFSKKCRLVKFSMVALVSATMAVTTV---
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                                     Conservative
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Query Match
Best Local Similarity
Matches 72; Conserv
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Cispecies: Listeria innoculary protein, probable lipoprotein lin0385 [imported] - Listeria innoculation protein lin0385 [imported] - Listeria innoculation by the cession a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a halfal constant a ha
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGSY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 K---WFFSDA-------KIQSILQESSKSEATTKQSKNDVIKINTDSDI 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 ĠYFKDISPNKQSGGŸGÅIPTĠFIMSNGQIVYPQĎNSNWSBITSEEBNRALTIDKDĠNL-- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
354 PESANEYEESD----FNPIPPPRQPSSMQTDFTLPSFQGDQAISAVDDVVSFYNSVN 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 RRVFSKKCRLVKFSMVALVSATMAVTTVTLENTAL-ARQTQVSNDVV---LNDGASKYLN
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22.6%; Pred. No. 1.3;
Live 42; Mismatches 118;
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Length 386;

DB 2;

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                                                                                                                                                                                                                                                                                                                    268 KLEPKPMVAGAMELLNEAATTKITGEEEAYSHTDLDDL-NANVEGSKVVYQAIIPALNAQ 326
                                                                                                                                                                  224 EADWIG--FHVIERALWEKKSLDGMD-----VYADKLLTDAKALQA----EVKNL 267
                                                                                                                                                                                                                                                                                              190 GGRDQ---KGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNAD----ELIPRAVVVSMQSS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----hYYKYV-TDQVDEFVAQTEIF 174
                                                                                                                                                                                                                  134 PAGWTGNPNHVKYKIEW----LNGLSYVGDFWNRSHLIADSLGGDALRVNAVTGTRTQNV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTLGTSQITPALFPKAGD------ILYSKLDELGRTRTARGTLTYANVEGSYG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --RDQKGGMR--YTEQRAQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 VKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKTRIVSSVTTTLLLGSILMNPVA------GAA-------DSDINI 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 06-592-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C;Accession: S69209
R;Hedengrahn, G.
Bubmitted to the BMBL Data Library, October 1992
A;Reference numbor: S69209
A;Reference numbor: S69209
A;Accession: S69209
A;Accession: S69208
A;Accession: S69208
A;Accession: S69208
A;Accession: S69208
A;Accession: S69208
A;Reference numbor: S69208
A;Reference numbor: S69208
A;Reference numbor: S69208
A;Residues: 1-319 <+RD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 EWLEANRDGYLYYEVAPIYNADELIPRAVVVSMOSSDNTINEKVLVYNTANGYTINY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : | | : : | : : | : : | NWGPYDRDSW-----NPVY-GNQLFMKTRNGSMKAADNFLDPNKASSLLSSGFSPDF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRQSFGKNQNPAGWTGNPNHVKYKIEWL-NGLSYVGDFWNRSHL-----IADSLGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: X01645; NID: 946763; PIDN: CAA25801.1; PID: 946765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93;
                          77;
                                                              35 TLENTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQI---
                                                                                                                                          TPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGSYGVRQSFG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 319;
                          88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fil. 26/Domain: signal sequence #status predicted <SIG>Fi27-319/Product: alpha-toxin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 18.2%; Pred. No. 2.1; 18.2%; Pred. No. 2.1; 4; Conservative 52; Mismatches 98;
      ed. No. 2.2;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-toxin precursor - Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                             DNTINEKV-LVYNTANGYTINYHNG 266
      20.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                 DKDLADQIDAAFNKMEDTLANYKNG 351
                                                                                                  131 SLDTLAKAKETKAKTSEVLDKAVD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 ALRVNAVTGTRTQNVGG-----
                          45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 18.23
Matches 54; Conservative
                          Conservative
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C; Keywords: toxin
Best Local Similarity
Matches 55; Conserv
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C;Accession: E83521
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathos A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                        A,Cross-references: GB:AE004532; GB:AE004091; NID:99946896; PIDN:AAG04383.1; GSPDB:GN001.
A,Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flagellin - Bscherichia coli (strain Su 1242)
C;Species: Bscherichia coli
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 26-Aug-1999
C;Accession: B48658;
C;Accession: B48658;
M;Schoenhals, G:; Whitfield, C:
J. Bacteriol: 175, 5395-5402, 1993
A;Title: Comparative analysis of flagellin sequences from Escherichia coli strains posse
A;Reference number: A48658; MUID:93374833; PMID:8366026
A;Accession: B48658
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        529 SRRVQFGFSSGIKRASYSLAVSRTQETGSFGRSDTQFTASVSIPLGGSARSSQVYANAVS 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ALRVN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   704 AVLPYMQPYRYNWVN------LDTNTLGSDTEISDSTQMAVPTRGAVIAKRFS 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQIT-------PALFPKAGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ----NEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRT-----RTARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 KADAAQTATVYTYNASAGNFSFSNVSNNTSA---KAGDVAASLLPPAGQTASGVYKAASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Residues: 1-595 <SCH>
A;Cross-references: GB:LO7387; NID:g290436; PIDN:AAA23797.1; PID:g290437
C;Superfamily: flagellin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 SRRV---FSKKCRLVKFSMVAL------VSATMAVTTVTLENTALARQTQV
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Best Local Similarity 21.5%; Pred. No. 6.5;
Matches 70; Conservative 51; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.7%; Score 95.5; DB 2;
Local Similarity 21.6%; Pred. No. 7.7;
les 58; Conservative 29; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 TGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: PA0994
C,Superfamily: outer membrane usher protein fimD
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-839 <STO>
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endo-arabinase related enzyme (family 43 glycosyl hydrolase domain and ricin B-like doma ('Species: Clostridium acetobutylicum C'Species: Clostridium acetobutylicum C'Accession: H96970 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 #S. Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4823-4838, 2001 #.Y.; Smith, D.R. A.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostrance.
285 EVNFDVDANGKITIGGQEAYLISDGNLTTNDAGGA-----TAATLDGLFKKAGDGQS 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                        -FWNRSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEW----- 208
                                                                 ---LEANRD------GYLYYEVAPIYNADELIPRAVVVSMQSSDNT-INEKVLVXNT 255
                                                                                                                                                   390 GTAVAANGDISATITYKSGVQTYQA--VFAAGD----GTASAKXADNTDVSNATATYTD 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Status: preliminary
A;Molecule type: DNA
A;Reduca: 1.676 <KUR>
A;Coss-teferences: GB:AE001437; PIDN:AAK78555.1; PID:g15023444; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
A;Gene: CAC0577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 TFNDSPNYYKTLGTSQITPAL-FPKAGDILYS------KLDELGRTRTARGTL-T 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 YANVEGSY-GVRQSFGKNQNPAGWTGNPNHVKYK-----IEWLNGLSYVGDFWNRSH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 LIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWL-----EANRD---- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 -ATDNFSGYHIRL-----FRSKNITG------PYTDAKGNPAICTSANDNKSNKGIKLF 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---TMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALAW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 KTNASDQYLGIKISGG-----YGTCGEGSYIVYDKATDYYYLYESYGGLD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 GYLYYEVAPIYNADELIPRAVVVSMOSSD--NTINEKVLVYNTANGYTINYHNGT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
6.6%; Score 93.5; DB 2; Length 676;
Best Local Similarity 21.7%; Pred. No. 8.5;
Matches 64; Conservative 47; Mismatches 93; Indels 9;
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Search completed: January 5, 2004, 18:42:51 Job time : 36.442 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

January 5, 2004, 15:46:12 Run on:

; Search time 22.9576 Seconds (without alignments) 555.120 Million cell updates/sec

US-08-482-785-8

Title: Perfect score:

1 MNLLGSRRVFSKKCRLVKFS......VYNTANGYTINYHNGTPTQK 271 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES		
Regult No.	Score	Query	Query Match Length	DB	ID	cript	
-	m	27.	327	-	DRN1 STREO	P26295 streptococ	
0	126.5	8.9	274		NUCE_STRPN	Q03158 streptococc	2000
m	104	7.3	392		PRTD_STRGR		nyce
4	100.5	7.1	1279	ч	APU THESA	ע	pu11
2	66	•	1861		APU_THETU		ou11
ø	95.5	٠	319		HLA STAAU	8	2000
7	94	9.9	341		OMPL PHOPR		cter
60	92.5	6.5	482	•	FLGE AQUAE	Ξ	aeo
σ	91.5	•	869		CFAC_ECOLI	_	chia
10	91	6.4			YQGS_BACSU		a su
11	88.5	6.2		ч	KIME_METJA	Q58487 methanococc	2000
12	88.5	6.2			GTFB_STRMU	P08987 streptococc	2000
13	88.5	6.2			POLN MANCV	_	ter
14		6.2		-	PAC ARTVI	P31956 arthrobacte	acte
15	•	6.2		Н	GUN_BACS6		ds s
16	~	6.2		ч	S	P27973 simian immū	immi
17	87	6.1		-		P02931 escherichia	chia
18	87	•	420	П			sns
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20	86.5	6.1	1116	П	RPOB_HETCA		igma
21		6.1	1709	Н	CHD1_HUMAN	O14646 homo sapien	ojen
22	96	6.1	288		BSN2_BACSU		3 Bu
23	96	6.1	296	-			comm
24	96	6.1	1182		RPOB_STAAU	P47768 staphylococ	2000
25	82	0.9	213	-			osis
56	82	6.0	420		DHE3_PYRAB	Q47950 pyrococcus	ene
27	82	6.0	524	ч	CK13 YEAST	P39962 Baccharomyc	эшус
28		9.0	1165	ч	RPC2_SCHPO	Q10233 schizosacch	acch
59	84.5	9	1723		PM20 CHLPN	Q9z812 chlamydia	la p
30	84	5.9	800		GUN BACS1	4	
31	84	5.9	1102	٦		P77965 synechocyst	yat
32		υ. ο.	1196	-		43	111
33	83.5	5.9	227	-	XYN1_HUMIN	P55334 humicola	ui e

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11 SKKCR--LVKFSMVALVS-ATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALAW

2 SKKLRNFLVRIIVAAFASFAVMAIPPYH-HNTVLAKTVSVNQ----

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68 TFNDSPNYYKTLGTSQITPALFPK-----

Query Match 27.2%; Score 385; DB 1; Length 327; Best Local Similarity 33.0%; Pred. No. 7.7e-26; Matches 100; Conservative 39; Mismatches 96; Indels 6

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108 TARGTLTYANVEGSYGVROSFGKNONPAGW-----TGN------PNH

43 TYGEYKDYYTVIGESNIDQSAFPKIYKTTERVYKGQGTSEKRVTVSDVVYNPLDGYKRST 102

QBnyy3 staphylococ P37898 saccharomyc Q2295 chlamydia p Q32896 chlamydia p P36917 thermoanaer Q65730 b genome po P07912 escherichia P34153 vibrio chol P38946 enterococcuc P17801 za mays (m O07642 cyanothece	AA.	e) late) (Streptodornase) (DNase).	Streptococcaceae	SEGUENCE FROM N.A. STRAIN=H46A; MEDLINE=203051; PubMed=1937032; MEDLINE=203051; PubMed=1937032; MOIINOWSKR R., Ceglowski P., Kok J., Venema G.; "Isolation, sequence and expression in Escherichia coli, Bacillus subtilis and Lactococcus lactis of the DNase (Gerreptodornase)-encoding gene from Streptococcus equisimilis H46A."; -I- FUNCTION: MAY BANC A ROLE IN S.EQUISIMILIS VIRULENCEI- CATALYTIC ACTIVITY: Endonucleolytic Cleavage to 5.	phosphodinucleotide and 5'-phosphooligonucleotide end-products. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	TIAL). LEASE. 'BEAAE7 CRC64;
HUTH STAAW AAPI-YEAST PWPI-CHLPN XYNA-THESA POLG BYTUI KBL ECOLI KBL SALTY KBL SALTY KRL ECOLI KRL SALTY KRYO MAIZE NIFD CYAAS	ALIGNMENTS	ted) Bequence update) annotation update) r (EC 3.1.21.1) (St	lis. Lactobacillales; St	32; Ok J., Venema G.; ssion in Escherichii s of the DNase Irom Streptococcus IN S.EQUISIMILE VII	hodinucleotide and 5'-phosphooligonuci Sa-PROT entry is copyright. It is produ- the Swiss Institute of Bioinformatics bean Bioinformatics Institute. There a non-profit institutions as long as i and this statement is not removed. Us, requires a license agreement (See http in email to license@isb-sib.ch).), Nuclease, Signal. OR 35 (POTENTIAL). DEOXYRIBONUCLEASE. 4 MW; 7529702FDEFBE4AF7
NEW HEER BY BY BY BY BY BY BY BY BY BY BY BY BY		Created) Last seç Last ann ursor (E	tobac	19370 P., K expre lacti gene ROLE	nd 5' copyr ute o cs In ituti nt is se ag	Nucl MW;
504 856 9422 3093 3998 666 666	STANDARD;	22, Creat 22, Last 36, Last precursor		Pubmed=1937032; llowski P., Kok nce and expressi coccus lactis o nncoding gene fr 991).	try is Instit iformatit insteme	06.1 06.1 24 27 3684
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334 335 337 337 338 33.5 33.5 33.5 33.5 33.5 33.5 33.5	J. 1 STREQ DRNI STREQ	1992 1992 1998 Donuc	Suc. Streptococcus equisimi Bacteria, Firmicutes, Streptococcus. NCBI_TAXID=119602,	SEQUENCE FROM N.A. STRAIN=H46A; MEDILINE=92039051; PubMed=1937035 WOLLINOWSKR R., Ceglowski P., Kok "Isolation, sequence and express subtills and Lactococcus lactis (streptodornase)-encoding gene i Gene 106:115-119(1991)	phosphodinucleotide and 5'-phosphool This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinforthe European Bioinformatics Institute. Use by non-profit institutions as lon modified and this statement is not removentities requires a license agreement (so or send an email to license@isb-sib.ch).	EMBL; X17241; CAAAS1 PIR; JT0584; JT0584. Hydrolaee; Endonucle SIGNAL 1 CHAIN 25 SEQUENCE 327 AA;
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                              163 VPVVLTTLKGKKYNSHLFVASHLFADSLGGKSIRKNAITGTQMQNVGTR--KGGMQYIEK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC BAA-255 / R6;
STRAIN=ATCC BAA-255 / PubMed=11544234;
HOBKINB J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., Hoskins J., Alborn W.E. Jr., Fritz L., Fu D.-J., Lagace R.E., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., Leblanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Morris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R., Jr., Skatrud P.L.,
                                                                                  VKYKI EMLNGLSYVGDFWNRSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQ
                                                                     RAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U. Bacteriol. 183:5703-5717(2001).

-i. FUNCTION: By degrading DNA that enters the cell, plays a role the competence of cells to be transformed.

-i. SUBGELLULAR LOCATION: Membrane-bound.

-i. SIMILARITY: Belongs to the DNA/RNA non-specific endonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN=ATCC BAA-334 / TIGR4;

MEDLINE-2155709; PubMed=11463916;

MEDLINE-2155709; PubMed=11463916;

Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,

Putin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,

Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.

Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,

"Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
115-SEP-2003 (Rel. 42, Last annotation update)
DNA-entry nuclease (Competence-specific nuclease) (EC 3.1.30.-).
ENDA OR SP1964 OR SPR1779.
Streptococcus preumoniae, and
Streptococcus pneumoniae, and
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the bacterium Streptococcus pneumoniae strain R6.";
                                                                                                                                                                                                                           274 AA
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90294291; PubMed=2359120;
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                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1313, 171101;
                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                              HNG 266
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 IGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPNYYKTLGTSQITPALFPKAGDILYSKLDE--LGRTRTARGTLTYANVEGSYGVRQSFG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 KNONPAGWIGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSL----GGDALR---VNAV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 İNLSOKKQASEAPSQALAESVLTDAVKSQIKGSLEWNGSGAFIVNGNKTNLDAKVSSKPY
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Sidhu S.S., Kalmar G.B., Willis L.G., Borgford T.J.;
"Protease evolution in Streptomyces griseus. Discovery of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
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PROSITE; PS01070; NUCLEASE NON SPEC; 1.
Competence; Hydrolase; Nuclease; Endonuclease; Signal-anchor;
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274 AA; 29890 MW; 59B2243F0150CD98 CRC64;
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21.9%; Pred. No. 0.0011;
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serine protease D precursor (EC 3.4.21.-) (SGPD).
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-!- SUBUNIT: Homodimer.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2A.
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                                                                                                                                                                                                         EMBL; X54225; CAA38134.1; -.
EMBL; AE007466; AAK76031.1; -.
EMBL; AE008543; AAL00582.1; -.
PIR; A99094; A99094.
PIR; F95229; F95229.
PIR; S10641; S10641.
TIGR; S1954; -.
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TRANSMEM 8 25 SIGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 LGADAAGSYY--DATAKTL--VVNVVDEAGAEOVR-----OAGGKARIVENSLAEL---K 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 TARGTLT-YANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHL 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 IADSLGGDALRVNAVTGTRTQNVGGRDQ-------KGGMRY-----TEQRA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 TSWSDTQGGSEIGANEGSSFPENDYGLVKYTSDTAHPSEVNLYDGSTQAITQAGDATVGQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 LKHRRISRKRATLAGSAVVALVAAGFTFQTANASDDVPAFGAKTLSADAAGKLATTLDRD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LGSRRVFSKKCRLVKFSMVALVSATMAVTTV------TLENTALAR-QTQVSND 50
                                                                                                                                                                                                                                                                                                                                                                                                                         88; Gaps
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1-JUN-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Amylopullulanase precursor (Alpha-amylase/pullulanase) [Includes: Apha-amylase (EC 3.2.1.1) (1,4-alpha-Delucan glucanohydrolase);
Pullulanase (EC 3.2.1.4) (1,4-alpha-Delucan glucanohydrolase)
(Alpha-dextrin endo-1,6-alpha-glucosidase)].
                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 0.15;
38; Mismatches 123; Indels
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CHARGE RELAY SYSTEM.
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CHARGE RELAY SYST
CHARGE RELAY SYST
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InterPro; IPR001216; EndopptdeeS2A.
InterPro; IPR001216; EndopptdeeS2A.
InterPro; IPR001216; EndopptdeeS2A.
InterPro; PR001254; Ser_protesse_Try.
Pfam; PR00809; trypsin; 1.
PR081TB; PR00801; ALYTICPTASE.
SMART; SM00020; Tryp SPC; 1.
PR0SITE; PS00134; TRYPSIN_ER; 1.
PR0SITE; PS001135; TRYPSIN_ER; 1.
PR0SITE; PS01125; TRYPSIN_ER; 1.
Pydrolase; Serine protesse; Symogen; Signis IRM STANDEN.
                                                                                                                                                                                                                                                                                                                                                                                                 7.3%; Score 104;
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                                                                                                         EMBL; L29019; AAA74409.1; -.
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                                                                                                                    PIR, A56123; A56123.
HSSP; P41140; 2SFA.
MEROPS; S01.266; -.
                                                                                                                                                                                                                                                                                                                                                                          392 AA;
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P36905;
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ACT_SITE
ACT_SITE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                STRAIN=B6A-RI;
MEDLINE=94161525; PubMed=8117096;
Ramesh M.V., Podkovyrov S.M., Lowe S.E., Zeikus J.G.;
Ramesh M.V., Podkovyrov G.M., Lowe S.E., Zeikus J.G.;
"Cloning and sequencing of the Thermoanaerobacterium saccharolyticum B6A-RI apu gene and purification and characterization of the amylopullulanase from Escherichia coli.";
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Thermoanaerobacter saccharolyticum.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacterium.
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION OF PROBABLE VECTOR CONTAMINATION
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735 73
1279 AA;
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                                                                                                                                               NCBI_TaxID=28896;
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ACT_SITE
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964 SSVEGGLYEKIASNVTGTTFEDTNVTNGLKYVYAISAVDELGNESEMSIDTVAYP---A 1019
                                                                                                 Y-----PIGWVGNLTQVVDNHVISVSNPTEDIYAEVWADGLTNSTGQGPNMIAQ 1068
                                                                                                                                                                                                     1069 LGYKYVGGTVN-----DSVYGSV--YNSVYGVDDSDFTWVNAQYVGDIGNNDQYKASLH 1120
                                                                                                                                                                                                                                                                                    1121 LINRSMGYLMRFSDNQGQSWTTTDT---LSFYVVP---SDDLIKPTAPILNQPGVESSRV 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=DSM 3896 / EM1;

MEDLINE=94252998; PubMed=8195085;

A Matuschek M., Burchhardt G., Sahm K., Bahl H.;

MEDLINE=94252998; PubMed=8195085;

A matuschek M., Burchhardt G., Sahm K., Bahl H.;

"Pullulanase of Thermoanaerobacterium thermosulfurigenes EM1

(Clostridium thermosulfurogenes): molecular analysis of the gene,

T composite structure of the enzyme, and a common model for its

attachment to the cell surface.";

J. Bacteriol. 176:3295-3302(1994).

-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

-!- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic

linkages in pullulan and in amylopectin and glycogen, and the
alpha- and beta-limit dextrins of amylopectin and glycogen.

-!- SUBCELJULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS AN

S-LAYER ANCHOR.
                                                                                                                                                   ----YVGDFWNRSHLIADSLGGDALRVNAVTGTRTQ-------NVGGRDQKGG---
                                                                                                                                                                                                                                                       -----VRYTEQRAQEWLEANRDGYLYYEVAPIYNADELI-PRAVV-----V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1994 (Rel. 30, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Amyloullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase
type II) [Includes: Alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucan glucanohydrolase) (Alpha-dextrin endo-1,6-alpha-glucana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                  --KYKIEWLNGLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 2 fibronectin type III domains. SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoanaerobacter thermosulfurogenes (Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermoanaerobacteriaceae; Thermoanaerobacterium.
NCBI_TaxID=33950;
                                                                                                                                                                                                                                                                                                                                                                                   1175 SLTWSPSTDN--VGIYNYEIYRSDGGTFN 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1861 AA
                                                                                                                                                                                                                                                                                                                                                      SMOSSDNTINEKVLVYN----TANGYTIN 262
                                               YGVRQSFGKNQNPAGWTGN----PNHV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR006589; Alp amyl_cat_sub.
InterPro, IPR006048; Alpha amyl_C.
InterPro, IPR006047; Alpha amyl_cat.
InterPro, IPR003961; FN_III.
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P38536;
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964 SVEGGLYEKIASNVTETTFEDANVTNGLKYVYAISAIDELG---NESGISNDAVAYPAY- 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     911 VPAMSGVMLISDDGQDLTA----PQAPSNVVVTSGNGKV---DLSWLQSDGATGYNIYRS 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 KGG-----MRYTEQRAQEWLEANRDGYLYYEVAPIYNADELI-PRAVVVSM-----
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                                                                                                                                                                SMART; SM00642; Aamy; 1.
SMART; SM00642; Aamy; C; 1.
SMART; SM00606; FN3; 2.
PROSITE; PS01072; SLH DOMAIN; 3.
Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; Repeat; Multifunctional enzyme; Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 VRQSFGKNQNPAGWTGN-----PNHV------KYKIEWLNGLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TINEKVLVY---NTANGYTINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.0%; Score 99; DB 1; Length 1861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D -> E (IN REF. 1; AAB00841)
                                                                                                                                                                                                                                                                                                                AMYLOPULLULANASE.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SLH 1.
SLH 3.
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01-MRE-1989 (Rel. 10, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Albha-hemolysin precursor (Alpha-toxin) (Alpha-HL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes, Bacillales, Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3.1;
39; Mismatches
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Glyco hydro 131g
                  Glyco_hydro_13N
SLH.
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                                                  Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02806; alpha-amylase_C; 1.
Pfam; PF02903; alpha-amylase_N; 1.
Pfam; PF002041; fin3; 2.
Pfam; PF02922; isoamylase_N; 1.
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1739 SLH
1803 SLH
1861 SLH
1734 D ->
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STRAINS SEQUENCE FROM N.A., AND SEQUENCE STRAINS WOOD 46;
MEDLINE=85053471; PubMed=6500704;
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Conservative
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HLY OR HLA.
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1248
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1861 AA;
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Best Local Similarity
Matches 75; Conserv
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                  nterPro, I
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P09616;
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us-08-482-785-8.rsp

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Walker B., Bayley H.;

"Key residues for membrane binding, oligomerization, and pore forming activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin in and taphylococcal alpha-hemolysin in Langar Bilayer in the membranic activity of staphylococcare activity of staphylococcare activity in the missence and activity of staphylococcare activity in the wisherders and the staphylococcare activity of staphylococcare activity of staphylococcare activity of staphylococcare activity and activity activity and activity activity and activity activity and activity activity and activity activity and activity activity and activity activity and activity activity and activity activity and activity activity and activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activit
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MEDLINE-94222552; PubMed-8168947;
Menzide B.E., Kernodle D.S.;
"Site-directed mutegenesis of the alpha-toxin gene of Staphylococcus
aureus: role of histidines in toxin activity in vitro and in a murine
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Wood 46 / ATCC 10832;
MBDININE=9710281; bubmed=8943190;
Song L., Hobaugh M.R., Shustak C., Cheley S., Bayley H., Gouaux J.E.;
"Structure of staphylococcal alpha-hemolysin, a heptameric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Histidine residues near the N-terminus of staphylococcal alpha-toxin as reporters of regions that are critical for oligomerization and
                Primary sequence of the alpha-toxin gene from Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93016135; PubMed=1400487;
Walker B., Krishnassetry M., Zorn L., Bayley H.;
Assembly of the oligomeric membrane pore formed by Staphylococcal alpha-hemolysin examined by truncation mutagenesis.";
J. Biol. Chem. 267:21782-21786(1992).
                                                                                                                                                                                                                                 Walker B., Krishnasastry M., Zorn L., Kasianowicz J., Bayley H.;
Functional expression of the alpha-hemolysin of Staphylococcus
arrens in intect Escherichia coli and in cell lysates. Deletion of
five C-terminal amino acids selectively impairs hemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGENESIS OF HISTIDINE RESIDUES.
MEDLINE=94245329; PubMed=8188346;
Vutrech R., Hildebrand A., Hobom G., Tranum-Jensen J., Ward R.,
Kehoe M., Bhakdi S.;
                                                                                                                                            Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                              SEQUENCE OF 27-319 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
STRAIN=Wood 46 / ATCC 10832;
                                                                                                                                                                                                                                                                                                      activity.";
J. Biol. Chem. 267:10902-10909(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nodel.";
Infect. Immun. 62:1843-1847(1994).
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MEDLINE=96032742; PubMed=7559447;
                                                                                                                                                                                                                  WEDLINE=92268149; PubMed=1587866;
                                                    Infect. Immun. 46:615-618(1984)
                                                                                      REVISIONS, SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane pore.";
Science 274:1859-1866(1996)
G.S., Kehoe M.;
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                                                                                                                                                                                             STRAIN=Wood 46
                                                                                                                           Hedengrahn G
                                                                                                         STRAIN=Wood
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                                                                                                                                                                                                                                                                                                                                                                                                                  H->L: NO OLIGOMERIZATION NOR HEMOLYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H->L: 7% OF NORMAL HEMOLYTIC ACTIVITY.
H->L: 16% OF NORMAL HEMOLYTIC ACTIVITY.
H->L: 46% OF NORMAL HEMOLYTIC ACTIVITY.
LENGTH, 26 ANGSTROMS IN DIAMETER) WHICH FORMS THE TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                             H->R: NO OLIGOMERIZATION NOR HEMOLYTIC
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                                                                                                                                                                                                                                                                                                                                                                                             CLEAVAGE OF MONOMERS BY PROTEINASE K (MAJOR SITE).
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CLEAVAGE OF MONOMERS BY PROTEINASE
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                                                                                                                                                                                                                                                                                                                                                               (MAJOR SITE).
CLEAVAGE OF MONOMERS BY PROTEINASE
                       SIMILARITY: BELONGS TO THE AEROLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                      ALPHA-HEMOLYSIN.
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                                                                                                                                                                                                                                                                                                                                         SITE)
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PROSITE; PS00274; AEROLYSIN; 1.
Hemolysis; Toxin; Signal; 3D-structure.
SIGNAL
                                                                                                                                                  EMBL, M90536; AAA26598 1; -.
PIR; S69209; S69209.
PDB; 7AHL; 14-JAN-98.
InterPro; IPR005831; Aer hem.
InterPro; IPR005830; Aer hem_leuk.
InterPro; IPR001340; Hemlyen_pore.
InterPro; IPR001340; Hemlyen_pore.
InterPro; IPR0013963; Staph bicn_txn.
Pfam; PF01117; Aerolyain; I.
PRINTS; PR01468; BICOMPNTOXIN.
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160
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341
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000
16-OCT-2001
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                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                        -----ILYSKLDELGRIRTARGTLTYANVEGSYG 123
                                                                                                                                                                                                                                                                                                                    124 VRQSFGKNQNPAGWTGNPNHVKYKIEWL-NGLSYVGDFWNRSHL------IADSLGGD 174
                                                                                                                                                                                                                                                                                                                                 93 VYSEBGANKSGLAW---PSAFKVQLQLPDNEVAQISDYYPRNSIDTKEYMSTLTYGFNGN 149
                                                                                                                                                                                                                                                                                                                                                                -----RDQKGGMR--YTEQRAQ 206
                                                                                                                                                                                                                                                                                                                                                                                    -----VTGDDTGKIGGLIGANVSIGHTLKYVQPDFKTILESPTDKKVGWKVIFNNMVNQ 203
                                                                                                                                                                                                                           17 VKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYY 76
                                                                                                                                                                                                                                         KT-GTIDIGSNITVKTGDLVIYDKENGMHKKVFYSFIDDKNHNKKLLVIRTKGTIAGQYR 92
                                                                                                                                                                                                                                                                                                                                                                                                                       204 NWGPYDRDSW----NPVY-GNQLFMKTRNGSMKAADNFLDPNKASSLLSSGFSPDF 254
                                                                                                                                                                                                                                                                                                                                                                                                          207 EWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pressure-regulated porin-like protein from the deep-sea bacterium shotobacterium species strain SS9.";
J. Bacteriol. 178:5027-5031(1996).
-1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96326353; PubMed=8759872; Welch T.J., Bartlett D.H.; "Isolation and characterization of the structural gene for OmpL,
                                                                                                                                                                              6.7%; Score 95.5; DB 1; Length 319;
18.2%; Pred. No. 0.62;
ive 52; Mismatches 98; Indels 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential).
-!- INDUCTION: IN RESPONSE TO ELEVATED HYDROSTATIC PRESSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Protecobacteria, Gammaprotecobacteria, Vibrionales, Vibrionaceae, Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (strain SS9)).
                                                                                                                                                         35904 MW; 6711C415DF7EBF30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Photobacterium profundum (Photobacterium
                                                                                                                                                                                                                                                                                                                                                                175 ALRVNAVTGTRTQNVGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porin-like protein L precursor
                                                                                                                                                                                                                                                                        KTLGTSQITPALFPKAGD---
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                 248
250
260
263
263
286
311
                                                                                                                                                316
319 AA;
                                                                                                                                                                                           Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOPR
                                                                                                                                                                                                                                                                       11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPNYYKTLGTSQITP----ALFPKAGDILYSKLDELGRTRTA------RGTLTYANVE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GSYGVROSF----GKNONPAGWIGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 GSLGMLTDFTDIMAYHGNEAG----NKLAAADRTDNNLSYVGSF------DLNGDN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 LTVKA-----NYVFGGSDENEGYSAAAMYAMDMGLGFGAGYGEQDGQSSKNGNEDKTGKQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRVRINVAGKTDITEDFYGVGFFEKEFSSADSDNDE---TRYAYAGVGSQYGQLVYGKAD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 MVALVSATMAVTTVTL-----ENTALARQTQVSNDVVLND--GASKYLNEALAWTFND 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LIALAVAAASISSVATAAEVYSDETSSLAVGGRFEARAVLADVNKDENVTNTASSEVSDK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRVNAVTGTRTQNVGGRDQKGGMR------YTEQRAQEWLEANRD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                 84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 AFGAISYTISDFYFSG-----LYQDSRNTVVNNDLIDESTGYEFAAAYT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 392:353-358(1998).
-!- SIMILARITY: BELONGS TO THE FLAGELLA BASAL BODY ROD PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLV-----YNTANGYT
                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                    L.
CRC64;
                                                                                                                                                                                                                                                PORIN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                  ED3D66A9F3DEB585
                  InterPro; IPR003229; OMP 2.
InterPro; IPR001702; PorIn Gram-ve.
Pfam; PF00267; Gram-ve.porins; 1.
ProDom; PD000808; OMP 2; 1.
Pransmembrane; Porin; Signal; Outer membrane.
stGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 39, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          6.6%; Score 94; DB 1; 23.9%; Pred. No. 0.91;
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MEDLINE=98196666; PubMed=9537320;
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PIR; B70460; B70460.
Interpro; IRR00144; Flag_bb_rod.
Pfam; PF00460; flg_bb_rod; 1.
                                                                                                                                                                                                                                                                                  341 AA; 36672 MW;
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FLGE OR AQ 1859.
Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
EMBL; U59311; AAB50064.1;
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                                                                                                                                                                                                                            109 -----TYYTRDGRFRI------136
                                                                                                                                                                                                                                                                                85 TEITTDLAIEGKALFILRDVL----- 108
                                                                                                                                                         45 TQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELG 104
                                                                                                                                                                                                             105 RTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRS 164
                                                                                                                                                                                                                                                              165 HLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPI 224
                                                                                                                               25 NLANANTVGFKKSRPIFQDMVSQVVVGLNTTTGTVKTTTFGAGAVVDSTQKVWTIGSFKQ 84
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The nucleotide sequence of the first two genes of the CFA/I fimbrial operon of human encerotoxigenic Escherichia coli."; Microb. Pathog. 6:297-309(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92239981; PubMed=1352712; Jordi B.J.A.M., Gaastra W.; Jordi B.J.A.M., Willshaw G.A., van der Zeijst B.A.M., Gaastra W.; Jordi B.J.A.M., Willshaw G.A., van der Zeijst B.A.M., Gaastra W.; The complete nucleotide sequence of region 1 of the CFA/I fimbrial operon of human enterotoxigenic Escherichia coli."; DNA Seq. 2.257-263(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MG-1992 (Rel. 23, Last annotation update)
CFA/I fimbrial subunit C precursor (Colonization factor antigen
                                                 6.5%; Score 92.5; DB 1; Length 482;
19.4%; Pred. No. 1.9;
ive 30; Mismatches 74; Indels 121;
                                                                                                     2 NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALA----
          Flagella, Complete proteomē. –
SEQUENCE 482 AA; 53568 MW; 10494DC9521A8762 CRC64;
                                                                                                                                                                                                                                                                                                                                     225 YNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Enterotoxigenic;
MEDLINE-89330163; PubMed=2569152;
Mamers A.M., Pol H.J., Willshaw G.A., Kusters J.G.,
van der Zeijst B.A.M., Gaastra W.;
PS00588; FLAGELLA_BB_ROD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M5561; AAC41416.1; -.
PIR; C56617; C56617.
                                                                            54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                              Best Local Similarity
Matches 54; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid NTP513
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CFAC_ECOLI
ID _CFAC_ECOLI
AC P25733;
PROSITE;
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117 NVEGSY-----GVRQSF----IEWLN 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 GLSYVGDFWN---RSHLIADSLGGDALRVNAVTGTRTQNV-GGRDQKGGMRYTEQRAQEW 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   489 TLGYSDTYSESVYKSHILSE-----YGFYNQNIYKGRTQR--WQLTSSTSLKW 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 LEANRDGYLYYEVAPIYNAD--ELIPR----AVVVSMQSSDNTINEKVLVYNTANGYTIN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunnet F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L.V., Caldwell B., Capuano V., Carter N.M., Broullet S., Bruschi C.V., Caldwell B., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Britach K.D., Errington J., Febret C., Ferrari B., Foulgar D., Britach K.D., Errington J., Febret C., Ferrari B., Foulgar D., Rritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Adim S.Y., Glaser P., Goffeau A., Golightly B.J., Granger D., Grandi G., Guy B.J., Haga K., Haich J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Arabita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Kotter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Amiliado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Persecan E., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolte C., Roche B., Roce M., Sadáie Y., Reiger M., Rivolte C., Roche B., Roce M., Sadáie Y., Satler B., Rappoort G., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F., Rock F.
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the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=168 / JH642;
MEDILTRE97124195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                             65;
                                                                                                                                                                                                                      6.5%; Score 91.5; DB 1; Length 869; 22.3%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                             46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                      CFA/I FIMBRIAL SUBUNIT C. EC4C626DA9B718B7 CRC64;
Antigen; Signal; Fimbria; Outer membrane; Plasmid.
SIGNAL 1 22 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                             32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98044033; PubMed=9384377;
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                                                                                           869 C
97830 MW;
                                                                                                                                                                        Hypothetical protein yqgS
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                                                                                           23 (
869 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sporulation genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 YHNG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 VILVSLEST---- OSFVINEKLNGEEITPFLNDFIKOSYNFNNVYHOT-GOGKTSDSEF- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 KAGDILYSKLDELGRTRTARGTLTYANVEGSYGVRQSFGKNONPAGWTGNPNHVKYKIEW 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 NVDNSLY----PLG-----RGAVFFTNAGNQYMAAPEILKN---SGYYSAVLHANNK--- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SFWNRD-LMYDSFGYDSFFDINSYDVTDENTVGWGLKDKE----FFEQSSE- 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 INGLSYVGDFWNRSHLIADSLGGDA-LRVNA--VTGTRTQNVGGRDQKGGMRYTEQRAQE 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VITVILENTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFP 90
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takenoki M., Tamakoshi A., Tamaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis",
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087; Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Gaps
                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.4%; Score 91; DB 1; Length 638; 23.8%; Pred. No. 3.7; ive 39; Mismatches 96; Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mevalonate kinase (EC 2.7.1.36) (MK).
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Subtilist; BG11866; yqgS.
InterPro; IPR000917; Sulfatase.
Pfam; PF00884; Sulfatase; 1.
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                                                                                                                                                                                                                            Nature 390:249-256(1997)
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Q58487;
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TRANSMEM
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Best Local
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Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.W. Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, methanococcus
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-i- MISCELLANEOUS: THERMOSTABLE; THE OPTIMAL TEMPERATURE FOR ACTIVITY IS 70-75 DEGREES CELSIUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphomevalonate.
--- COFACTOR: MAGNISIUM.
--- ENZYME REGULATION: FARNESYL- AND GERANYL-PYROPHOSPHATES ARE COMPETITIVE INHIBITORS. INHIBITED BY HIGH CONCENTRATION OF ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
MEDLINE=99428387; PubMed=10497066;
Huang K.-X., Scott A.I., Bennett G.N.;
"Overexpression, purification, and characterization of the thermostable mevalonate kinase from Methanococcus jannaschii.";
Protein Expr. Purif. 17:33-40(1999).
-!- CATALYTIC ACTIVITY: ATP + (R)-mevalonate = ADP + (R)-5-
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PROSITE; PS00627; GHMP KINASES ATP; 1.
Transferase; Kinase; ATP-binding; Magnesium; Complete proteome;
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InterPro; IPR00114; Galkinase.
InterPro; IPR005204; GHMP kinase.
InterPro; IPR006203; GHMPkinse ATP.
InterPro; IPR006205; Mev_gal Kin.
InterPro; IPR006205; Mev_gal Kin.
InterPro; IPR006206; Mev_galkinase.
Pfan, PF00288; GHMP kinases; 1.
PRINTS; PR00959; MEVGALKINASE.
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PIR; F64435; F64435.
PDB; 1KKH; 27-MAR-02.
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Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

-1- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEWTAL PLAQUE BECAUSE OF THE DEWTAL PLAQUE BECAUSE.

-1- FUNCTION: PRODUCTION OF BACTERIAL CELLS AND FOOD DEBRIS.

-1- CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl}(N+1).

-1- SUBCELLULAR LOCATION: Secreted.
-1- DISEASE: DEWTAL CARIES.
-1- MISCELLANEOUS: GTF-1 SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,5-LINKADES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS.
-1- ALINKED GLUCOSE AND SOME 1,6-GLUCOSE), GTF-S SYNTHESIZES BOTH FORMS OF GLUCANS.
-1- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-BINDING PROTEIN FROM S.MUTANS.
-1- SIMILARITY: Contains 10 cell wall binding repeate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseablesib.ch)
TRIQNVGG------RDQKGGMR-----YTEQRAQEWLEANRDGYLYYEVAP 223
                   SEQUENCE FROM N.A.
STRAIN-UALS9 / ATCC 700610 / Serotype C;
MEDLINE-22295063; PubMed=12397186;
Ajdic D., McShan W.W., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome aequence of Streptococcus mutans UALS9, a cariogenic dental
                                                                                                                                             GTFB STRMU STANDARD; PRI; 1476.AA.
P08987; O69381; O69387; O69396;
01-NOV-1988 (Rel. 09, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glucosyltransferase-I precursor (EC 2.4.1.5) (GTF-I) (Dextransucrase)
GSUCTOSE 6-Glucosyltransferase).
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S
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STRAIN=MT4239 / Serotype C, MT4245 / Serotype E, MT4251 / Serotype
MT4467 / Serotype E, and MT8148 / Serotype C;
MEDLINE=98231643; PubMed=9570124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fullwara T., Terao Y., Hoshino T., Kawabata S., Ooshima T., Sobue Kimura S., Hamada S.; "Molecular analyses of glucosyltransferase genes among strains of
                                                                                                                                                                                                                                                                                                                                                                  Shiroza T., Ueda S., Kuramitsu H.K.; "Sequence analysis of the gifB gene from Streptococcus mutans."; J. Bacteriol, 169:4263-4270(1987).
                                                                                                                                                                                                                                                                      Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, Streptococcus.
                                                                    210 | | | | : : | | : | | 232
                                                     224 IYNADELIPRAVVVSMQSSDNTINEKVLVYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus mutans.";
FEMS Microbiol. Lett. 161:331-336(1998).
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87308013; PubMed=3040685;
                                                                                                                                                                                                                                                            Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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A -> T (IN STRAIN MT4239).
S -> N (IN STRAIN MT4239).
H -> Y (IN STRAIN MT4251).
E -> K (IN STRAIN MT9148).
Y -> C (IN STRAIN MT9148).
A -> P (IN STRAIN MT9148).
R -> P (IN STRAIN MT9148).
R -> P (IN STRAIN MT9148).
Y -> H (IN STRAINS GS-5, MT4467).
AND MT9148).
S -> G (IN STRAINS GS-5, MT4239, MT4467).
AND MT9148).
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STRAIN MT4251).
STRAINS GS-5, MT4245, MT4251,
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Y -> H (IN STRAINS GS-5, MT4239, MT4467
AND MT8148).
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R -> A (IN REF. 1).
ADQDVRVAASTAPSTDGK -> LIKMFALRLARPHQQMA
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AND MT8148).
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SV -> NT (IN STRAINS GS-5, MT4239 AND
                                                                                   EMBJ, AEO14940, AANSB705.1, -.
InterPro; IPR002479; CW binding.
InterPro: IPR003318; G17co hydro 70.
Pfam; PF01473; CW binding 1.
Pfam; PF01473; CW binding 1.
Pfam; PF02324; G17co hydro 70; 1.
Transferase; G1ycosyltransferase; Signal; Repeat; Dental caries;
                                                                                                                                                                                                                                                                                                                                               7 -> 1 (IN STRAIN MT4239).
7 -> 1 (IN STRAIN GS-5).
MT4467 AND MSTRAINS GS-5, MT4245, M
MT4467 AND MSTRAIN MT4251).
Q -> P (IN STRAIN MT4251).
MT4467 AND MT8148).
S -> F (IN STRAIN MT4251).
K -> N (IN STRAIN MT4251).
K -> N (IN STRAIN MT4251).
K -> N (IN STRAIN MT4239).
N -> R (IN STRAIN MT4239).
I -> T (IN STRAIN MT4239).
I -> T (IN STRAIN MT4239).
F -> Y (IN STRAIN MT8148).
T -> I (IN STRAIN MT8148).
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GLUCAN-BINDING (APPROXIMATE)
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H -> L (IN REF. 1).
W; 9C6E09F731B4CBCF CRC64;
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M17361, AAA88588.1;
D88651; BAA26101.1;
D88654; BAA26105.1;
D88656; BAA26105.1;
D88666; BAA26113.1;
D89977; BAA26113.1;
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                                                                                                                                                                                                   1296 NGYAVTGARTINGQHLYFRANGVQVKGEFVTDRHGRISYYDGNSGDQIRNRFVRNAQGGW 1355
                                                                                                                                                                                                                                                                                                                                  1356 FYFDNNGYAVTGARTINGGHLYFRANGVQVKGEFVTDRYGRISYYDSNSGDQIRNRFVRN 1415
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                                                                                                                                                                                                                                                                                                       209 LEANRDGY-----LYYEVAPIYNADELIP----RAVVVSMQSSDNTINEKV-- 250
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                                                                ----YKTLGTSQITPALFPKAGDI
                                                                                   1121 LSNGLOLRDAILKNEDGTYAYYGNDGRRYENGYYQFMSGVWRHFNNGEMSVGLTVIDGQV
                                                                                                                     LYSKLDELGR-----TRTARGTLTYANVEGSYGVROSFGKN------ONPAGWTG-
                                                                                                                                                                               ---NPNHVKYKIEWLNGLSYVGDF-WNRSHLIA--DSLGGDALRVN-------
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manchester virus (Human enteric calicivirus).
Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-1- SIMILARITY: TO PICORNAVIRUS POLYPEPTIDES.
-1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
02-SP-FBE-2003 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: RNA-directed RNA polymerase
(EC 2.7.7.48); Thiol protease 3C (EC 3.4.22.-); Helicase (2C like protein); Coat protein].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=95390791; PubMed=7661689; Lambden P.R.;
Liu B.L., Clarke I.N., Caul B.O., Lambden P.R.;

"Human enteric calicitieses have a unique genome structure and ax distinct from the Norwalk-like viruses.";

Arch. Virol. 140:1345-1356(1995).

-I FUNCTION: P2C IS IMPORTANT IN RNA REPLICATION (BY SIMILARITY).

-I FUNCTION: THE CYSTEINE PROTEASE IS THE PROTEASE RESPONSIBLE FOR THE POST-TRANSLATIONAL PROCESSING OF THE POLYPEPTIDE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                 Indels 105;
    DB 1; Length 1476;
                                107;
                 ; Pred. No. 18;
36; Mismatches
                                                        47 VSNDVVLNDGASKYLNEALAWTFNDSPNY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2208 AA.
    Score 88.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                    ----LVYNTANGYTI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X86560; CAA60262.1; -.
                              67; Conservative
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                Similarity
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Interpro; IPR004005; Calici coat. Interpro; IPR004004; Calici pol hel Interpro; IPR000317; Endoptase C24.

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-----WVQGPFSQLPHMQIGSGSPVYFTTRLHPVFTI-----SEGTFETPNI---TV 1079
                                                                                                                                                                                                                                                                                                                                                                                                                        143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 YTEQRAQEWLEANRDGYLYYEV---APIYNADELIPRAVVVSMQSSDNTINEKVLVYNTA 256
                                                                                                                                                                                                                                                                                                                                                                                                            102 ELGRIRIARGILIYANVEGSYGVR-------OSFGKNONPAG---WIGNPNH
                                                                                                                                                                                                                                                                                                                                                                                                                                           936 BIRAMRMAGGAYTHATIIGRGGVRDEIIRTSPRRAPTRPQQHYEEEGFTAIVEFTQGGDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 VKYKIEWLNG----LSYVGDFWNRSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JJJ-1993 (Rel. 26, Created)
01-JJJ-1993 (Rel. 26, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Penicillin G acylase precursor (EC 3.5.1.11) (Penicillin G amidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           996 IGYGVHIGNGNVITVTHVAS-----TSDEVNGSAFKITRTVGETT-----
                                                                                                                                                               Polyprotein; Transferase; RNA-directed RNA polymerase; Hydrolase; Thiol protease; Helicase; ATP-binding; Coat protein. ? ? HELICASE (P2C-LIKE).
                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 2208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Micrococcineae, Micrococcaceae, Arthrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A BETA CHAIN
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Extracellular (Potential)
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY $45.
                                                                                                                                                                                                                                                                                                                                                                                  £ 29
                                                                                                                                                                                                                                                                                                                                                                                  29; Mismatches
                                                                                                                                                                                                                                                                                                                                                  Score 88.5; I
Pred. No. 31;
InterPro; IPR000605; RNA helicase, InterPro; IPR00105; RNA_pol_DS_PS. InterPro; IPR001205; RNA_pol_P3D. InterPro; IPR001205; RNA_pol_P3D. InterPro; IPR001054; RNA_pol_Psvir. Pfam, PF00815; Calici coat; I. Pfam; PF00810; RNA_bol; I. Pfam; PF00910; RNA_helicase; I. PRINTS; PR00916; ZGENDOPTASE. PRINTS; PR00916; ZGENDOPTASE.
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                                                                                                                                                                                                                                                                                                                                                                 19.5%;
                                                                                                                                                                                                                                                                                                                                                                               38; Conservative
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2208 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        618 EWWNNLHDKLFMDELGDFYGITKEITDHRYGASLAYKNISKESTNYKWVNVDQEKIIMES 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ADEL----IPRAVV-----VSMQSSD----NTINEKVLVYN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -AGWIGNPNHVKYKIEWLNG-LSYVGDFWNRSHLIADSLGGDALR------VNAVIGIR
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-I- CAPALATTC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucans.

-I- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL HYRROLASES).

-I- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
     is in
                                                                                                                                                                                                                                                                                                                                                                    PENICILLIN G ACYLASE ZYMOGEN.
PENICILLIN G ACYLASE ALPHA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                            SPACER PEPTIDE.
PENICILLIN G ACYLASE BETA SUBUNIT.
BY SIMILARITY.
9863E58C526C85D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88; Indels 110;
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DILY-----SKLDELGRIRIARGILIYANVEGSYGVROSFGKNONP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 88; DB 1; Length 802;
Pred. No. 9.1;
     as its content
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Bacillus sp. (strain KSM-635).
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                       InterPro, IPR002692, Penicil_amidase.
Pfam; PF01804, Penicil_amidase, 1.
Hydrolase, Antibiotic Fesistance, Zymogen, Signal.
SIGNAL 124 POTENTIAL.
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41; Mismatches
institutions as long
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234
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  non-profit
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PROSITE; PS01072; SLH_DOWAIN; 2.
Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat; 3D-structure.
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1 Similarity 20.7%; Pred. No. 12;
63; Conservative 36; Mismatches 124; Indels
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PDB; 1G01, 31-DEC-02.
PDB; 1G0C; 31-DEC-02.
INTERPO; IPR005086; CBM 17 28.
INTERPO; IPR001547; GIYCO_FYGEN, PF03424; CBM 17 28; 2.
Pfam; PF001424; CBM 17 28; 2.
Pfam; PF00155; Cellulase; 1.
Pfam; PF00155; SLH; 3.
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SPECIES=S.pyogenes; STRAIN=C203S; MEDLINE=21233066; PubMed=11335140; Gerlach D., Schmidt K.H., Fleischer B.; Gerlach D., Schmidt K.H., Fleischer B.; "Basic streptococcal superantigens (SPEX/SMEZ or SPEC) are responsible for the mitogenic activity of the so called mitogenic factor MF."; FEMS Immunol. Med. Microbiol. 30:209-216(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIESS. Pyogenes; STRAIN=MGAS315 / Serotype M3; MEDLINE=22133808; PubMed=12122206; Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S., Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Schlievert P.M., Musser J.M.; Groom sequence of a serotype M3 strain of group A Streptococcus: Dhage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Streptodornase B precursor (Mitogenic factor 25K).
DNASEB OR MF OR SPYM3_1745.
Streptococcus pyogenes, and
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             emergence.";

proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)

EMBL; A2055272; CAC35734.1; -.

EMBL; AE014170; AAM80352.1; -.
Signal; Complete proteome.

SIGNAL

42

CHAIN

STREPTODORNASE B.
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Q8XTL2
Q9LR37
Q8D6V8
Q8G2H7
                Q8E067
Q8E6B6
Q8E0P2
Q8VT23
Q8VT23
Q9X721
Q9X721
Q9X8E4
Q9R4B2
Q9R4B2
Q9ZL61
Q8XTM0
                                                                                                                                                                  09A012
09ZQL7
09ZHU7
09ZHU6
099QC6
08VSL2
097FU6
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QBREKO atreptococc
QBNZ16 atreptococc
Q33735 streptococc
Q93ccl atreptococc
Q8469 atreptococc
Q93mn6 lactobacill
Q84m1 atreptococc
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Copyright (c) 1993 - 2004 Compugen Ltd.
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STRAIN=SF370 / ATCC 700294 / Serctype M1;
MEDLINE=21192649; PubMed=11296296;
MEDLINE=21192649; PubMed=11296296;
MEDLINE=21192649; PubMed=11296296;
Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Nadjar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R., Song L., White J., "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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                                                                                                                                       1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY
                                                                                                                                                               1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY
                                                                                            Gaps
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"Cloning, characterization and overexpression of a Streptococcus
pyogenes gene encoding a new type of mitogenic factor.";
FEBS Lett. 331:187-192(1993).
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                                             Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 02, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mitogenic factor precursor (Mitogenic factor, 25K).
MF OR SPY2043 OR SPYM18 2104.
Streptcoccus pyogenes, and
Streptcoccus pyogenes (serctype M18).
Bacteria, Firmicutes; Lactobacillales; Streptcoccaceae,
                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A novel cloning method used arbitrarily primed PCR.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
  8FD8849E3CD01352 CRC64;
                                          100.0%; Score 1418; DB 16;
100.0%; Pred. No. 6.3e-103;
ive 0; Mismatches 0;
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  30090 MW;
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  271 AA;
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                                                                  Similarity
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    SEQUENCE
                                             Query Match
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Q54969;
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MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Bares S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Rammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
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"Genome sequence and comparative microarray analysis of serotype Migroup A Streptococcus strains associated with acute rheumatic fever outbreaks.";
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                                                                                                                                                                                                                                                                                                                                                          Length 271;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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EMBL; AE014158; AAM'9702.1; -.
Complete proteone; Hypothetical protein.
SEQUENCE 264 AA; 29333 WW; 6E395486BA309399 CRC64;
                                                                                                                                                                                                                                                                                                        271 AA; 30062 MW; 8FD89DA38A124352 CRC64;
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                                                                                                                                                                                                                                                                                                                                                        Score 1414; DB 16;
Pred. No. 1.3e-102;
0; Mismatches 1;
                                                                                                    Acad. Sci. U.S.A. 99:4668-4673(2002)
                                                                                                                                                                                                                                                                                   MITOGENIC FACTOR
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EMBL; AB006625; AAX34710.1; -.
EMBL; AS0100113; AAL98563.1; -.
Nuclease; Signal; Complete proteome.
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                                                                                                       Proc. Natl. Acad. Sci. U. 8
EMBL, D13428; BAA02693.1;
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Best Local Similarity 99.6
Matches 270; Conservative
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                          FNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGSYGVRQSF 128
                                                                                   --GKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNAVTGTRT 186
                                                                                                                                          QNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTI 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAINEMEDASS22 / Serotype M18;
MEDLINE-21927593; PubMed=11917108;
SMCOU J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.,
"Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 332;
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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EMBL. AEQ10084; AAL98274.1; -.
Complete protecome.
SEQUENCE 332 AA; 37652 MW; SBDC9F930865FBCO CRC64;
                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                      332 AA.
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NEKVIVYNVANGYTIDYNQGT 259
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PNYYKTLGTSQ1-----TPALFPKAG------DILYSKLDELGRTRTARGT 112
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Hasegawa T., Torii K., Hashikawa S., Iinuma Y., Ohta M.;

"Cloning and characterization of the deoxyribonuclease sdalpha gene
from Streptococcus pyogenes.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF410852; AAL02116.1; -.
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=serotype M49;
PodbeilBki A.;
Submitted (FBB-1995) to the EMBL/GenBank/DDBJ databasee.
                                                                                                                                                                                                                                                                                                                                                                                                                              streptococcal DNase gene (sdab).";
Infect. Immun. 64:5349-5356(1996).
EMBL; X84793; CAA59264.1; -.
SEQUENCE 385 AA; 43476 MW; 14922B0AFC3BD6D5 CRC64;
                                    Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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385
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EQUENCE FROM N.A.
STRAIN=serotype M49;
MEDLINE=97101060; PubMed=8945587;
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PRELIMINARY;
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01-JAN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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Best Local Similarity
Matches 96; Conserv
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NCBI_TaxID=1314;
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NCBI_TaxID=1314;
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53 LLP--FTANYQLQLGELDNLN----RATFSHIQLQDRHETKDVRTKINYDPVGW---- 100
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                                        VKYKIEWINGLSYVGDFWNRSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQ 203
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                                                         24 LVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQ
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                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.";
Submitted (DBC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF461500; AAL66371.1; -.
SEQUENCE 252 AA; 28347 MW; 92CABBC832F5CFB8 CRC64;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
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69; Conserv
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                                                                                     11 SKKCR--LVKFSMVALVS-ATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALAM
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                                                          Gaps
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STRAIN=MGAS315 / Serotype M3;
MEDLINE=22131808; bubMed=1212206;
MEDLINE=22131808; bubMed=1212206;
Mammarella W.D., Liu W.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
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                              Length 327;
                                                                                                       95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
8treptodornase (Sdn)-phage associated.
SDN OR SPYN3 1409.
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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 62DDD3443017071F CRC64;
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EMBL, AE014163; AAM80016.1; -
Complete proteome.
SEQUENCE 326 AA; 36645 MW; C9635F8A0CA6ASIF CR
                            27.4%; Score 389; DB 2; 33.0%; Pred. No. 2.1e-22;
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Best Local Similarity
 327 AA;
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EMBL; AE006523; AAK33665.1;
EMBL; AE010008; AAL97446.1;
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                                                                                                                                                                                                          38 NTALARQT------QVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQIT 85
                                                                 Alpert C.-A., Zagorec M.;
"Phyalcal and genetic map of the Lactobacillus sakei 23K chromosome.";
"Phyalcal and genetic map of the Lactobacillus sakei 23K chromosome.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF400065; AAK92009.1;
SEQUENCE 278 AA; 30597 MW; DBA1337649DEBBAD CRC64;
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STRAINS=SF370 / ATCC 700294 / Serotype M1;

MIDDLINE=21192684; Pubmed=11296596;

Ferretti J.G., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorcov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                              Dudez A.-M., Chaillou S., Hissler L., Stentz R., Champomier-Verges M.,
Alpert C.-A., Zagorec M.;
                                                                                                                                                                                                                                                                                            -----FSNLDQLNRAGTANALLN----KSMMPTAKREGLTWNPTGW----RNKR
                                                                                                                                                                                                                                                                                                                      146 YKIEWLNGLSYVGDFWNRSHLIADSLGGDALR-VNAVTGTRTQNVGGRDQKGGMRYTEQR
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STRAIN=MGAS8232 / Serotype M18;

STRAIN=MGAS8232 / Serotype M18;

STRAIN=MGAS8232 / Serotype M18;

STRAIN=MGAS933 / Serotype M18;

STRAIN=A1927593; PubMed=11917108;

SMOOT J.C., Barbian D.E., Ricklefs S.M., Porcella S.F.,

Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,

RAPUR V., Dally J.A., Veasy L.G., Musser J.M.;

"Genome sequence and comparative microarray analysis of serotype M18

group A Streptococcus strains associated with acute rheumatic fever

outbreaks.";

Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative DNase (Similar to mitogenic factor), phage associated
                                                                                                                                                      DB 2; Length 278;
                                                                                                                                                                                34; Mismatches 80; Indels
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Streptococcus pyogenes (serotype M18).
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
                                                                                                                                                    13.1%; Score 185.5; DB 2 26.5%; Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                Similarity 26.5: 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1314, 186103;
                                                                                                                                                                                                                                                                                                                                                                                                                                   259 YTINYHNGT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 VTLNYADGS 273
                                       SEQUENCE FROM N.A
Lactobacillus.
NCBL_TaxID=1599;
                                                                                                                                                                                                                                                                                            124
                                                                                                                                                                                                                                                                                                                                                                             205
                                                                                                                                                    Query Match
                                                                                                                                                                    Local
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                                                                                                                                                                                Matchee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 ITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGSYGVRQSFGK-NQNPAGWTGNPN 142
                                                                                                                                                                                                                                                                                                                                                                                                                               HVKYKIEWLNG--LSYVGDFWNRSHLIADSLGG--DALRVNAVTGTRTQNVG---GRDQK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 H-NYOFPYGDGSKSSWV---MNRGHLVGYQFCGLNDEPR-NLVAMTAWLNTGAYSGANDS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 G--GMRYTEORAOEWLEANRDGYLYYEVAPIYNADELIPRAV-------VVSM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 LVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQ
                                                                                                                                                                                                                                                      -----ANTHYKNTVSSK
                                                                                                                                                                                                                                                                                                                                                                    53 LLP--FTANYOLOLGELDNIN-----RATFSHIOLODRHETKDVRTKINYDPVGW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 VGDFWNRSHLIADSLGGDALRV-NAVTGTRTONVGGRDOKGGMRYTEORAQEWLEANRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 YDNLDFLNRVGVABAMLGKBLMPKB--ARQDI-SSVKPTGWKNK-----KITFNGKQDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-NEM316 / Serctype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease."; mol. Microbiol. 45:1499-1513(2002). EMBL; AL766845; CAD46026.1; -. EMBL; AL766846; CAD46556.1; -. EMBL; AL766848; CAD46656.1; -.
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                                                                                12.9%; Score 182.5; DB 16; Length 252; 24.6%; Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 266;
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                          252 AA; 28373 MW; 71EA2332E358440D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 protein; Complete proteome.
266 AA; 30394 MW; D07DEEF65BF006A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
                                                                                                                                        93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 QSSDNTINEK----VLVYNTANGYTINYHNGTPTQK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 NSNKESIDENGVTTVILENSAPNINLDYLNGTATPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83;
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31.2%; Pred. No. 1.1e-05;
ive 21; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                        48; Mismatches
                                                                                                                                                                                                                              |: ::::||:|::
LLLLSLSITTITVDAARVRTYPNVSH-----
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Best Local Similarity 31.2%
Matches 54; Conservative
                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                             Local Similarity
Complete proteome.
SEQUENCE 252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=216495;
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134

53

QBPOB6;

RESULT 12

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----TPGILPFTGSYQLVLGDLDNLQRP-----TFAHIQLKDQDEPNIKRK-GLKFNP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 AGWIGNPNHVKYKIEWLNGLSYVGDFW--NRSHLIADSLGG--DALRVNAVTGTRTQNVG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 PGW-----H-NYKLTDANGKT----TWLMDRGHLVGYQFSGLNDEPK-NLVTMTKYLNTG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --NPVGW-----H-NYNFYYKKSDGSIGKMWLMARGHLVGYQF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 MVALVSATMAVITVTLENTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bolotin A., Wincker P., Mauger S., Jaillon O., Malaxme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis ILJ403.",
EMBL, AB06253; AAK04254.1;
EMBL, AB06253; AAK04254.1;
EMPLOTHELICAL DICTERIAL COMPLETE PROTECTION.
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Seazte S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.S., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
                                                                                                                                                                                                                                                                                                                                                                                TSQITPALFPKAG--DILYSKLDELGRIRTARGTLTYANV----EGSYGVRQSFGKNQNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 TYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFW--NRSHLIA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 DSLGGDALRV-----NAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 GRDQKG-GMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 TENDSPNYYKTLGTS-QITPALFPKAGDILYSKLDELGRT-----
                                                                                                                                                                  268 AA; 30398 MW; 24EA4762A5DDAA5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, Complete proteome.
33 AA; 28854 MW; EAA95B6FA317207C CRC64;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                      85;
                                                                                                                                                                                                           11.4%; Score 161.5; DB 1
25.6%; Pred. No. 9.4e-05;
:ive 36; Mismatches 83
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Pred. No. 0.00039
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10.8%; Score 153.5;
Best Local Similarity 24.4%; Pred. No. 0.00
Matches 60; Conservative 26; Mismatches
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01-JUN-2001 (TrEMBLrel. 17
01-MAR-2002 (TrEMBLrel. 20
Hypothetical protein ybfB.
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                 Similarity
                                                                                                                                               Complete proteome.
SEQUENCE 268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 TSQITPALFPKAG--DILYSKLDELGRTRTARGTLTYANV----EGSYGVRQSFGKNQNP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 MVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TPGILPFTGSYQLVLGDLDNLQRP-----TFAHIQLKDQDEPNIKRK-GLKFNP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 PGW-----H-NYKLTDANGKT----TWLMDRGHLVGYQFSGLNDEPK-NLVTMTKYLNTG
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13 VVILIAILTTFTTSTVTAARKIRNFPDTTBILLGTKATE----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chaussee M.S.,
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Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.,
"Genome sequence and comparative microarray analysis of serotype MIS
group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202
                       267
                                           GRDQKG-GMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSD
                   216 YLYYEVAPIYNADELIPRAVVVSMQS-SDNTINEKVLVYNTANGYTINYHNGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.4%; Score 161.5; DB 16; Length 266; 25.6%; Pred. No. 9.3e-05;
                                                                                                                                                                                                                                                                                     SPYM18_1446.
Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927931; Pubmed=11911108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 AA; 30153 MW; 45475BC64C408F9A CRC64;
                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                    266 AA
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STRAIN=SF370 / ATCC 700294 / Serotype M1;
MEDLINE=21192684; PubMed=11296296;
                                                                                                                                                                                                           Created)
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                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AC10063; AAL98024.1;
Complete proteome.
SEQUENCE 266 ".
                                                                                                                                                                                                         (TrEMBLrel. 22, (TrEMBLrel. 22, (TrEMBLrel. 22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=186103;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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NCBI_TaxID=1314;
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01-JUN-2001
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51 VVLNDGASKYLNEALAWTFNDSPN---YYKTLGTSQITPALFPKAGDILYSKLDELGRTR 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 -MDRGHLVGYQFSGMNNVPENLVTWTKYLNTGFSENNPDGMLYYENRLDSWLANHKNFWL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 TARGILIYANVEGSYGVROSFGKNO---NPAGWIGNPNHVKY----KIEWLNGLSYVGD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 FWNRSHLIADSLGG-DALRVNAVTGTRTQNVG-GRDQKGGMRYTEQRAQEWLEANRDGYL 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=NEM116 / Serotype III;
MEDLINE=2224508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
Kunst F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513 (2002).
BMBL, AL766844, CAD45798.1; -.
Sagaist; gbs0153; -.
Hypothetical protein; Complete proteome.
SEQUENCE 343 AA; 38877 MW; 11BF35A12D959DF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
10.6%; Score 150; DB 16; Length 343;
Best Local Similarity 25.5%; Pred. No. 0.001;
Matches 62; Conservative 33; Mismatches 102; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Hypothetical protein.
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250 NYADGT 255
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NCBI_TaxID=216495;
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New DNA encoding Streptococcus pyogenes DNase B - for diagnosing S. pyogenes infection, also new promoter for expressing other proteins
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AAB66308
ABU02468
AAR88824
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DNA-ase-B; diagnostic;
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                                                     18-MAY-1994;
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Mitogenic factor a
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Recombinant DNaseB
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                 January
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Streptococcus poly

1220 1220 1216 1214 1195 258 253 202 171.5

Score

Rebult No.

mutans glucosyl mutans glucosyl mutans glucosyl

Streptococcus muta Staphylococcus epi

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Gaps

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DB 16; Length 293; Indels

100.0%; Score 1220; DB 16; 100.0%; Pred. No. 2.5e-120; ive 0; Mismatches 0;

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RSHLIADSLGGDALRVNAVTGTRTONVGGRDQKGGMRYTBQRAQBWLEANRDGYLYYBVA 180
                                                                                                                                                                                                                                                                                                                   45 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYXKTLGTSQITPALFPKAGDILVSKLDE 104
                                                                                                                                                                                                                                                                                                                                                                         LGRIRTARGILIYANVEGSYGVRQSFGKNQNPAGWIGNPNHVKYKIEWLNGLSYVGDFWN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ROTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
                                                                 The sequence shows a gene product corresponding to a Streptococcus pyogenes DNA-ase-B. The protein is useful as a diagnostic agent, vaccine or as an aerosol to trea excessive lung viscosity, e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 229
                                                                                                                               cystic fibrosis. (Updated on 25-MAR-2003 to correct PN field.)
                                 Disclosure, Fig 5; 97pp; English.
                                                                                                                                                                                                                                                                 Matches 229; Conservative
                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                       293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200234771-A2
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Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP30017;
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proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ROTOVSINDVALNDGASKYLNEALAWIFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 60
                                                                                                                                                                                                                                                                                                       1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
                                                                                                                                                                                                                                                                       Gaps
                                                                             The protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding Streptococcus pyogenes DNase B - for diagnosing S. pyogenes infection, also new promoter for expressing other
                                                                           DNA-ase-B, which is a marker of S. pyogenes infection. The prote may be used as a diagnostic agent or vaccine for S. pyogenes, or may be used as an aerosol to treat excessive lung viscosity, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 229
                                                                                                                                                                                                                               Length 229;
                                                           This is the full-length sequence of Streptococcus pyogenes
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-ase-B; diagnostic; vaccine; cystic fibrosis therapy.
                                                                                                                                                                                                                             Score 1220; DB 16;
Pred. No. 1.7e-120;
; Mismatches 0;
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                                                                                                                                   in cystic fibrosis.
(Updated on 25-MAR-2003 to correct PN field.)
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/note= "mature protein"
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                         Claim 1; Fig 4; 97pp; English.
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                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 229; Conservative
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                                                                                                                                                                                             229 AA;
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15-AUG-1995
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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Margarit Ros YI,
                                                                                                                                                                              Streptococcus polypeptide SEQ ID NO 9210
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A
ABP30017 standard; Protein; 271
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes.
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N-PSDB; ABN70648.
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Adams CW,
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       The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
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                                                                                                                                                                                                                                                                                       RQTQVSNDVVLNDGASKYLNEALAWTFNDSFNYYKTLGTSQITPALFPKAGDILYSKLDE 102
                                                                                                                                                                                                                                                                                                                                                                                  RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEAA 222
                                                                                                                                                                                                                                                                                                                      LGRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 120
                                                                                                                                                                                                                                                                                                                                           LGRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 162
                                                                                                                                                                                                                                                                                                                                                                RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unawe B; nuclease; cystic fibrosis; vaccine; immunoassay; diagnosis; Escherichia coli.
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                               Score 1216; DB 23;
Pred. No. 5.8e-120;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pyogenes strain ATCC 14289

    S. pyogenes DNaseB and leader sequence.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44..271
/label= Mat_protein
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                                                                                                                                                                                                                               99.7%;
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                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.6
Matches 228; Conservative
                                                                                                                                                                                     Streptococcus proteins
                                                                                                                                                                                                           271 AA
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                                                                                                                                                                                                            Seguence
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43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 180
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                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes DNase B, including the leader peptide, has the amino acid sequence given in AAR8881. The enzyme can be obtd. on a large scale by expression of encoding DNA (AAT12774) in transformed host cells, esp. Escherichia coli. Inclusion of the leader peptide facilitates purification of the recombinant enzyme. The DNase B is useful in immunoassays to detect anti-bNase B antibodies in serum as a marker for S. pyogenes infection, and is also useful as a vaccine or for treatment, via aerosol delivery, of cystic fibrosis.
                                                                                                                                                       New DNA encoding Streptococcus pyogenes DNase B - for recombinant prodn. of the enzyme in other bacteria, useful in immunoassays or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hara A, Hinuma Y, Igarashi H, Iwasaki M, Kishishita M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitogenic factor associated with group A Streptococci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.5%; Score 1214; DB 17;
99.6%; Pred. No. 9.4e-120;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                  Claim 1; Page 67-70; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR58702 standard; Protein; 271 AA.
Pang PPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        delayed hypersensitivity; ss
                                                                                                                                                                                                                         for treating cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93JP-0037383
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.6
Matches 228, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes
                                                              WPI; 1996-151377/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 AA;
                                                                                            N-PSDB; AAT12774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
29-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP613947-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR58702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Gaps

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Length

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New DNA encoding Streptococcus pyogenes DNase B - for recombinant prodm. of the enzyme in other bacteria, useful in immunoassays or for treating cystic fibrosis
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                                                                                                                          The sequence represents the N-terminal fragment of Streptococcus pyogenes DNA-ase-B, which is a marker of S. pyogenes infection. The protein may be used as a diagnostic agent or vaccine for S. pyogenes, or may be used as a diagnostic agent or vaccine for S. pyogenes, or may be used as a diagnostic agent or vaccine for S. viscosity. e.g. in cystic fibrosis.

(Updated on 25-MAR-2003 to correct PN field.)
New DNA encoding Streptococcus pyogenes DNase B - for diagnosing S. pyogenes infection, also new promoter for expressing other proteins
                                                                                                                                                                                                                                                                                                                                                                                            43 ROTQVSNDVVINDGASKYINEALAWTFNDSPNYYKTLGTSQITPALFPK
                                                                                                                                                                                                                                                                                                                                                                         1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNase B; nuclease; cystic fibrosis; vaccine; immunoassay; diagnosis; Escherichia coli.
                                                                                                                                                                                                                                                                                                21.1%; Score 258; DB 16;
100.0%; Pred. No. 2.5e-19;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes strain ATCC 14289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S. pyogenes DNase B partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..43
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 3; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pang PPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR88821 standard; Protein; 90
                                                                                                Claim 3; Fig 3; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US09450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US09450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams CW, Belei MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-151377/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT12773
                                                                                                                                                                                                                                                                   91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9606174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-FEB-1996.
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR88821;
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
AAR88821
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                              FFFXSXSSSSSSSXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGRITRIARGILIYANVEGSYGVROSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŔSHLIADSLGGDALRVNAVTGTRTONVGGRDOKGGMRYTEORAQEWLEANRDGYLYYEAA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
                                                                                                                                                                                                                              AAREBTO2 shows a mitogenic factor which exhibits rabbit peripheral blood lymphocyte mitogenicity and/or DNA hydrolysing activity. It is strongly associated with group A Streptococci and the nucleotide sequences can be used for the microdetection of the gene and provide an early diagnosis of infectious disease caused by the bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 229
                                                                                                                                                                                                                                                                                                                                                                                                                   98.0%; Score 1195; DB 15; Length 271; 98.3%; Pred. No. 9.6e-118; ive 2; Mismatches 2; Indels 0
                                                                                                                       New mitogenic factor gene from Streptococcus pyogenes - used develop prods. for the early diagnosis of infectious disease caused by gp A streptococci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-ase-B2 N-terminal fragment; diagnostic; vaccine; cystic
                                                                                                                                                                                                                                                                                                                              (See also AAQ71613-26).
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                     Claim 7; Page 12-13; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR70700 standard; Protein; 91 AA
                                  Yutsudo T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pang PPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-ase-B2 N-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US05626.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
                                  Takeda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams CW, Belei CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-052087/07.
N-PSDB; AAQ85036.
                                                                         WPI; 1994-272994/34
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibrosis therapy
                                                                                          N-PSDB; AAQ71612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9500650-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
14-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-1995
                                      Okumura K,
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR70700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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RESULT 6 AAR70700

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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Streptococcus protein for the treatment or prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for detecting a compound that binds to the protein -
                  Streptococcus polypeptide SEQ ID NO 3962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 3550; 4525pp; English.
                                                                                                                                                                                                                                                                                           29-OCT-2001; 2001WO-GB04789.
                                                                                                                                                                                                                                                                                                                                     27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                          Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-352536/38.
N-PSDB; ABN68024.
                                                                                                                                                                                                    WO200234771-A2
                                                                                                                                                                                                                                                 02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Telford J,
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The N-terminal sequence (AAR88825) of a Streptococcus pyogenes arecombinant Dawse B expressed in Escherichia coli transformants was detd. A modified Dasse B gene (AAT12780) was produced by PCR amplification of the native DNase B gene (AAT12774) in clone lambda 2-6. The gene was inserted into vector del-33 for expression in E. coli. Modification of the gene resulted in the presence of an additional Arg residue at the DNase B V-terminus (see also AAR88824).
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA encoding Streptococcus pyogenes DNase B - for recombinant prodn. of the enzyme in other bacteria, useful in immunoassays or
                                                                                                           ö
                                                                                                                                                        48
                                                                                                                                                                                                90
                                                               Length 90;
                                                                                                                                                                             43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFP
                                                                                                                                                   RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cystic fibrosis; vaccine; immunoassay;
                                                                                                         Indels
                                                                                                           ö
                                                               Score 253; DB 17;
Pred. No. 8.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.6%; Scott No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%; Pred. No. 0.100.0%;
                                                                           100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNaseB N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6, Page 48; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosia; Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                            AAR88825 standard; Peptide; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US09450
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                         48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Belei MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-151377/15.
                                                   Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNase B; nuclease;
                90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9606174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                          AAR88825;
                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Fraser

Grandi G,

Masignani V, Margarit Ros YI,

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenee), comparising one of 5481 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 PAGWIGNPNHVKYKIEWLNG--LSYVGDFWNRSHLIADSLGG--DALRVNAVIGTRIQNV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 YYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGSYGVRQSFGK-NQN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 HYKNTVSSKLLP--FTANYQLQLGELDNLN-----RATFSHIQLQDRHETKDVRTKINYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G---GRDQKG--GMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23; Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 -----VVSMQSSDNTINEK----VLVYNTANGYTINYHNGTPTQK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 SGELLTIRLNSNKESIDENGVTTVILENSAPNINLDYLNGTATPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.1%; Score 171.5; DB 23; 27.6%; Pred. No. 1.6e-09; ive 37; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 27.6 see 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Indels

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ABP27393 standard; Protein; 252

02-JUL-2002 (first entry)

ABP27393;

ABP27393 ID ABP2 XX AC ABP2 XX DT 02-J

RESULT 9

Length 38;

Score 202; DB 17; Pred. No. 5.6e-14;

Local Similarity 100. es 38; Conservative

Matches

ઠ 용 9

ABP25596

ABP25596

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FNPPGW-----H-NYKLTDANGKT----TWLMDRGHLVGYQFSGLNDEPK-NLVTMTKYL 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 SGLNNEARNLVPETAWFNGGNFTGTNDGNT-----ASMLYYENRLDSWLANHPNYYLDY 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDNSSQVSTKSLASSVKQAPLTFKNQRQMVMANTDALGRAVDSHIQLKDSQEPKVKREPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYANVEGSYGVROSFGKNONPAGWIGNPNHVKYKIEWLNGLSYVGDFW--NRSHLIA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---NAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 EVAPIYNADELIPRAV---VVSMQSSDNTINEK-------VL-VYNTANGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 QVTPLYEGNELLPRQIRLAYVGIDKNGQTLSIKLGGGREKSGNGGATVVVLDNVAPNAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleotide sequence useful in the identification or Lactococcus lactis and related species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention is related to a Lactococcus lactis nucleotide
                                                NVGGRDQKG-GMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSD
                                                                                              NTGFSDKNPLGMLYYENRLDSWLALHPNFWLDYKVTPVYHKNELVPRQVVLQYVGID
                                                                                                                                                                                                                                                                                                                                                                                                                Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23; Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFNDSPNYYKTLGTS-QITPALFPKAGDILYSKLDELGRT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.;
85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.6%; Score 153.5; DB 3 ilarity 24.4%; Pred. No. 1.4e-07 Conservative 26; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; SEQ ID No 162; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Renault P,
                                                                                                                                                                                                                      ABB53460 standard; Protein; 263
                                                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis protein ybfB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis IL1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 DSLGGDALRV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2807446-A1
                                                                                                                                                                                                                                                                                                                      16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bolotine A,
66
                                                146
                                                                                                                                                                                                                                                                      ABB53460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
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                                                                                                                                                                        RESULT 11
                                                                                                                                                                                               ABB53460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 543 sequences (S1), given in the greptococcus pyogenes), comprising one of 543 sequences (S1), given in the greptococcus pyogenes), comprising one of 543 sequences (S1), given in cativity (I), nucleic acids encoding (I), ABN66044-ABN1526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a composition comprising (I) are used to detect of the composition comprising (I) are used to detect of a compound binds to composition comprising (I) are used to a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be manigitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromosophy, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                        Streptococcus, GAS, GBS, group B straptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial, antilnflammatory, infection, vaccine, meningitis, gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONPAGWIGNPNHVKYKIEWLNGLSYVGDFW--NRSHLIADSLGG--DALRVNAVIGIRIQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 LGTSQI-TPALFPKAG--DILYSKLDELGRTRTARGTLTYANV----EGSYGVRQSFGKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --
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V Streptococcus protein for the treatment or prevention of infedisease caused by Streptococcus bacteria, such as meningitis, detecting a compound that binds to the protein -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.0%; Score 158.5; DB 23; 31.1%; Pred. No. 4.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Margarit Ros YI,
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                                                                                                                                                                                                                                            Streptococcus polypeptide SEQ ID NO 368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 3190; 4525pp; English
                                                                                              ABP25596 standard; Protein; 268 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABN66227
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200234771-A2
                                                                                                                                                                                          02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32-MAY-2002
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Sequence Query Match

Local Matches 249

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA05803 to AAA05872 encode proteins, polypeptides and peptides (given in AAY91275 to AAY91343) isolated from Group B Streptococcus (GBS), also known as Streptococcus agalactiae. The GBS polymucleotides and polypeptides have antibacterial activity. Immunogenic compositions and for the treatment or prophylaxis of GBS infection. The polymucleotides and polypeptides can also be used as vaccines polymucleotides and polypeptides can also be used in the detection of GBS and for screening DNA encoding bacterial cell envelope associated or secreted antigens in gram positive bacteria. AAA05873 to AAA05941 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 NQNPAGW--TGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALR-----VN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 NWKPLGWHQVATNDHYGHAVD------KGHLIAYALAGNNFKGWDASVSNPQN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 AVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNAD-ELIPRAVVVS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Group B Streptococcus protein, useful as vaccine, for diagnosis of Streptococcal infections and for screening of antibodies or affibodies
                                                                                                                                                                                                                                                                                                                                         Group B Streptococcus, Streptococcus agalactiae, protein antigen, vaccine, screening, immunogen, detection, diagnosis, infection, antibody, affibody, antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.0%; Score 134.5; DB 21; Length 25.8%; Pred. No. 1.4e-05; Live 25; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                               Group B Streptococcus protein sequence SEQ ID NO:71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 MOSSDNTINEKVLVYNTANGYTINYHNGTPT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanniffy SB;
                                                                                                                                                           AAY91338 standard, Protein, 262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MICR-) MICROBIAL TECHNICS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-0016335.
99US-0125163.
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                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus agalactiae.
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220 NYHNGT 225
                                          250 NYADGT 255
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19-MAR-1999;
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the appecification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABM66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Nucleic acids encoding (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to detecmine whether a compound binds to used as a vaccine or dispositic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 LKTTPVGW-----H-NFKFYYNDGTQKA---WLMSRGRLICHQFSGLNNERKNLVPMTNW 139
                                                                                                                                                                                                                                                                                                            Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 QNVGGRDQKG-----GMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 YKTKENGTLP---FKHKRQLVLGELDDKGRA-----TFAHIQ--LKVKDEPKKKRVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NPAGWIGNPNHVKYKIEWLNGLSYVGDFW--NRSHLIADSLGG-DALRVNAVIGTRI
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                                                                                                                                                                                                                                                                                                                                               group A streptococcus; Streptococcus pyogenes; antibacterial; antinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Masignani V, Margarit Ros YI, Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                 Streptococcus polypeptide SEQ ID NO 3960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 3550; 4525pp; English.
ABP27392 standard; Protein; 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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(GENO-) INST GENOMIC RES
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les 56; Conserv
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Tettelin H;
                                                                           ABP27392;
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be thereafted the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the 
140 LNTGNYNSTNSSNPESMLFYEKQLKTWLSTHKNYYLDYKVTPIYQNNELIPRKIELKYVG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus, GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
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Streptococcus proteins.
                                                                               200 SDNT-----INEK------VLVYNTANGYTINYHNG 224
                                                                                                                      200 IDKTGKLLPIFIGNKSTQDQFGISTVTLENTSPNATIDYLSG 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus polypeptide SEQ ID NO 1300.
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                                                                                                                                                                                                                                                                   ABP26062 standard; Protein; 157 AA
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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INST GENOMIC RES.
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N-PSDB; ABN66693.
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Tettelin H,
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comparising one of 5483 sequences (31), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABM6604-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to detect streptococcus in a biological sample. (I) is used to detect streptococcus in a biological sample. (I) are used to detect streptococcus in a biological sample. (I) are used to recombinantly produce (I), may be streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity or produce of prometography, immunoassays, and distinguishing/identifying
       ----ALRVNA 138
                                                                                                   139 VTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNAD-ELIPRAVVVSM 197
                                   NWKPLGWHQVATNDHYGHAVD------KGHLİAYALAGNFKGWDASVSNPQNV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy
NQNPAGW--TGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGD--
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                                                                                                                                                                                       KSODGTLEFNVAIPNTQASYTMDYATGEIT 155
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                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus polypeptide SEQ ID NO 9324.
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                                                                                                                                                                                                                                                                                  ABP30074 standard; Protein; 261
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus agalactiae.
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(GENO-) INST GENOMIC RES.
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Tettelin H;
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Length 157;

10.7%; Score 131; DB 23; Length 1: 26.0%; Pred. No. 1.5e-05; Live 25; Mismatches 60; Indels

Query Match Best Local Similarity 26.0% Matches 39; Conservative

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                        Query Match 10.7%; Score 131; DB 23; Length 261; Best Local Similarity 26.0%; Pred. No. 3.3e-05; Matches 39; Conservative 25; Mismatches 60; Indels 26; Gaps
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Search completed: January 5, 2004, 18:38:09 Job time : 60.0424 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-107-532A-6904
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Maximum DB
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APPLICANT: Pang, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Relea, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
            PCT - US95 - 16126 - 1

US-09 - 793 - 293 - 35

US-09 - 285 - 991A - 305 9

US-09 - 071 - 035 - 404

US-09 - 071 - 035 - 402

US-09 - 071 - 035 - 402

US-09 - 108 - 452A - 579

US-09 - 206 - 942 - 47

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US-09 - 515 - 039 - 69

US-08 - 737 - 716 - 14

US-08 - 480 - 604A - 7

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US-08 - 495 - 136 - 7
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/393,889
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasaddana
STATE: California
                                                                                                                                                                                                                       US-08-957-310-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 795-6321
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH. 229 amino acids
                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08393889
Patent No. 6420152
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11.0.1.EKISTICS: 229 amino acids TOPOLOGY: 11.0.1.
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MEDIUM TYPE: Floppy disk
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Length 229;

100.0%; Score 1220; DB 4; 100.0%; Pred. No. 2.3e-122;

Query Match Best Local Similarity

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Sequence

ORGANISM: Streptococcus pyogenes

ORIGINAL SOURCE:

US-08-393-889-9

TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO

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43 RQTQVSNDVVLNDGASKKILNEALAWIFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 102
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                                                                                                                                                                         1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
                                              61 LGRITKTARGTLITYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWN
                                                                                                                                     121 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA
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                                                                                                                                                                                                                                                                                                                         181 PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IITLE OF INVENTION: Recombinant DNase B Derived from TITLE OF INVENTION: Streptococcus pyogenes NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INPORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFRENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
INFORMATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08393889
Patent No. 6420152
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Adams, Craig W. APPLICANT: Pang, Patty P.-Y APPLICANT: Belei, Marina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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: USA
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STATE: Californi
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SULT 3
-08-393-889-8
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                                                                                                                                                                                                                        RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 180
                                                                                                                    RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 60
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0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ); DB 5;
2.3e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Beckman Instruments, Inc.
APPLICANT: 2500 Harbor Boulevard
APPLICANT: 710-700 Harbor Boulevard
APPLICANT: Fulleston, California 92634
TITLE OF INVENTION: Recombinant DNase B Deriv
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCES: 16
CORRESPONDENCES: 16
CORRESPE: 2500 Harbor Boulevard
STREET: 2500 Harbor Boulevard
CITY: Fullerton
STREET: California
COUNTRY: USA
ZIP: 92634
COMPUTER REABABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1220;
100.0%; Pred. No. 2.3
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0; Mismatches
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REGISTRATION NUMBER: 26,769
REFERENCE/DOCKET NUMBER: 39D-1357 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application PC/TUS9409450 GENERAL INFORMATION:
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Matches 229; Conservative
   229; Conservative
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US-08-393-889-15
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                                                                  223 PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
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100.0%; Pred. No. 3e-122;
tive 0; Mismatches 0; Indels
                                                                                                                                                        PCT-US94-09450-8
Sequence 8, Application PC/TUS9409450
GENERAL INFORMATION:
APPLICANT: Beckman Instruments, Inc.
APPLICANT: 2500 Harbor Boulevard
APPLICANT: Packman instruments 92634
TITLE OF INVENTION: Recombinant DNase B Derived from TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: May, William H. 26,769
REGISTRATION NUMBER: 26,769
REFERENCE/DOCKET NUMBER: 39D-1357 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  E: Beckman Instruments, Inc
2500 Harbor Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-UN-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.
Matches 229; Conservative
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92634
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RESULT

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45 QTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDEL 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 SHLIADSLGGDALRVNAVIGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAP 224
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                                                                                                                                                DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Beckman Instruments, Inc.
APPLICANT: 2500 Harbor Boulevard
APPLICANT: Fullerton, California 92634
TITLE OF INVENTION: Recombinant DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.6%; Score 1215; DB 4;
100.0%; Pred. No. 1e-121;
tive 0; Mismatches 0;
                                        GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Adams, Craig W.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Deriv
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                             ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
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PCT-US94-09450-15
Sequence 15, Application PC/TUS9409450
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Application US/08393889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
                                                                                                                                                                                                                                                                                                                                                              ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 272 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (818) 795-632
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) MOLECULE TYPE: protein US-08-393-889-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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PCT-US94-09450-6
                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 GRIRTARGILIYANVEGSYGVROSFGKNONPAGWIGNPNHVKYKIEWLNGLSYVGDFWNR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 GRTRTARGTLITYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWINGLSYVGDFWNR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 SHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 SHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAP 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 OTQVSNDVVLNDGASKYLNBALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDEL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 IYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTOK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 IYNADELIPRAVVVSMQSSDNIINEKVLVYNTANGYTINYHNGTPTQK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 272;
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                                                                                                                                                   COUNTRY: CITIONIA

ZIP: 92634

ZIP: 92634

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-ANG-1994
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INPORMATION:
NAME: May, William H.
REGISTRATION NUMBER: 26, 769
REFERENCE/DOCKET NUMBER: 39D-1357 PCT
TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
TELECOMMULICATION 1995-4000
TELEFRAME (818) 795-6321
INPORMATION POR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08393889
Patent No. 6420152
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Relei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from NUMBR OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.6%; Score 1215; DB 5; 100.0%; Pred. No. 1e-121; tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
TITLE OF INVENTION: Streptococcus pyogenes
                           NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Pullerton
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 272 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / MOLECULE TYPE: protein
PCT-US94-09450-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-08-393-889-6
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COMPUTER READALE FORM:
MEDIUM TYPE: RIOPEPY disk
MUNIUM TYPE: RIOPEPY disk
COMPUTER: READALE FORM:
MEDIUM TYPE: RIOPEPY disk
COMPUTER: READALE FORM:
MEDIUM TYPE: RIOPEPY disk
COMPUTER: READALE FORM:
MEDIUM TYPE: RIOPEPY disk
COMPUTER: READER: READER: ROWNER: US/08/193,889
FILIND DATE:
READER: READER: ROWNER: US/08/193,889
FILIND DATE: READER: ROWNER: US/08/193,889
FILIND DATE: READER: ROWNER: US/08/193,889
FRICK RAPEL/CATION HUMBER: US/08/193,889
FRICK RAPEL/CATION HUMBER: US/08/193,889
FRICK RAPEL/CATION HUMBER: US/08/193,889
FRICK RAPEL/CATION HUMBER: US/08/193,889
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FRICK RAPEL/CATION HUMBER: US/08/193,889
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FRAGWER: TYPE: REPETCO.
ORGANIZABLE SOURCE: REPETCO.
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ORGANIZABLE SOURCE: REPETCO.
ORGANIZATION SYNTEM: PC-COSYDATION.
ORGANIZATION SYNTEM: PC-COSYDATION.
ORGANIZATION SYNTEM: READALE.
OCHERE SADDALE: PURCH.
ORGANIZATION SYNTEM: READALE.
OCHERE SADDALES: READER.
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Sequence 5038, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                        Gaps
                                                                        .;
0
                            ch 13.9%; Score 170; DB 4; Length 32; 1 Similarity 100.0%; Pred. No. 2.1e-11; 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 32;
                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-UNA-1993
ATYONEY/AGENT INFORMATION:
NAME: May, William H.
REGISTRATION NUMBER: 26,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1e-11;
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                                                                                                                2 QTQVSNDVVLNDGASKYLNEALAWTFNDSPNY 33
                                                                                                                                                         1 QTQVSNDVVLNDGASKYLNEALAWTFNDSPNY 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.9%; Score 170; DB
100.0%; Pred. No. 2.1
tive 0; Mismatches
                                                                                                                                                                                                                                                          Sequence 16, Application PC/TUS9409450 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 2500 Harbor Boulevard
CITY: Fullerton
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                       RESULT 10
PCT-US94-09450-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                    Score 202; DB 5; Length 38;
Pred. No. 1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/08393889
Patent No. 6420152
GENERAL INFORMATION:
APPLICANT: Adam, Patry P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROTOVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                 Query Match
16.6%; Score 202; DB
Best Local Similarity 100.0%; Pred. No. 1e-:
Matches 38; Conservative 0; Mismatches
REGISTRATION NUMBER: 26,769
REFERENCE/DOCKET NUMBER: 39D-1357 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEPAX: (818) 795-4321
INFORMATION POR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                             MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
PCT-US94-09450-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATE
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Parber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 32 amino acida
amino acid
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    California
                                                                                                                                                                           amino acid
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ORGANISM: Str
US-08-393-889-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-08-393-889-16
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Query Match

8.7%; Score 106; DB 4; Length 23;
Best Local Similarity 95.7%; Pred. No. 8.8e-05;
Matches 22; Conservative 0; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Beckman Instruments, Inc.
APPLICANT: E360 Harbor Boulevard
APPLICANT: Fullerton, California 92634
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF SECURNICS: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
STREET: 2500 Harbor Boulevard
TITLE OF CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09450
FILING DATE: 18-AUG-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,845
FILING DATE: 23-JUM-1993
ATTORNEY/AGENT INFORMATION:
NAME: MAY, WILLIAM H:
                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QTQVSNDVVLNDGASXYLNBALA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 OTQVSNDVVLNDGASKYLNEALA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERRENCE/DOCKET NUMBER: 9521
TELECOMUNICATION INFORMATION:
TELEFRONE: (818) 795-4301
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 23 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r: peptide
NO
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Fullerton
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL:
                                                                91001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US94-09450-4
                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-393-889-4
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ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 NAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :||||: | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Paray, Party P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                          NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                     COMPUTATION USA
ZIP: 02354
COMPUTATION OSA
COMPUTATION TYPE: CD/ROM ISO9660
COMPUTATION SYSTEM: «UNKNOWN>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 MQS-SDNTINEKVLVYNTANGYTINYHNGTPTQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AESIEDKKIEFNVFIYNVQDGYTINYETGQATK 94
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: 225 South Lake Avenue, Ninth Floor
Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAWE: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE FOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEFRONE: (781)893-5007
TELEFRAX: (781)893-5007
TELEFRAX: (781)893-5007
TELEFRAX: (781)893-5007
TELEFRAX: (781)893-5007
TELEFRAX: (781)893-6277
INFORMATION FOR SEQ ID NO: 5038:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: misc feature

; LOCATION: (B) LOCATION 1...97

; SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

US-09-107-532A-5038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                            STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08393889
Patent No. 6420152
                                                                                                                                                                          CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-393-889-4
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156 NLLGSHNFYPHRYSGLGYEHFVFCSEKFRKYNLNTMAFVNSQSAEFGPWPTQDGLCTLED 215
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                                                                                                                                                                                                                                                                                                                                               98 --DLSFFHKMGAYGVRLDIGFTGAEEAKMTRNPFGIKIEINMSSGTNYVDNIMSYSPNTD 155
                                                                                                                                                                                                                                                                                                                                                                                           127 DSLGGDALRVNAVTGTRTQNVGGRDQK-----GGMRYTEQRAQE---W-----LEA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GYLY-----YEVAPIYNADELIPRAVVVSMQSSDN 202
                                                                                                                                                                                                               11 INDGASKYLNEALAWTFNDSPNYYKTLGTS---QITPALFPKAGDILYSKLDELGRTRTA
                                                                                                                                                                                                                                             Query Match 7.8%; Score 95.5; DB 4; Length 379; Best Local Similarity 22.0%; Pred. No. 0.076; Matches 56; Conservative 37; Mismatches 91; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%; Score 91.5; DB 2; Length 869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Scott, June R.
APPLICANT: Frochlich, Barbara
APPLICANT: Caron, Judy
TITLE OF INVENTION: CS2 Proteins and Coding Sequences
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,101
FILING DATE: 07-101-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 6-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
             ; LOCATION: (B) LOCATION 1...379
; SEQUENCE DESCRIPTION: SEQ ID NO: 6904:
US-09-107-532A-6904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08483101
Patent No. 5932715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 T--ERICLFDNFHSY 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 TINEKVLVYNTANGY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (303) 499-8089
FPORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 869 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 80303
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US-08-483-101-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Sequence 6904, Application US/09107532A
Patent No. 6583275
GENERAL INPORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERABEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.7%; Score 106; DB 5; Length 23; Best Local Similarity 95.7%; Pred. No. 8.8e-05; Matches 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 QTQVSNDVVLNDGASKYLNEALA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTQVSNDVVLNDGASXYLNEALA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 379 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6904:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                       N-terminal
                                                                                                                                                                                     LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PC
                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-107-532A-6904
                                                                                                                                                                                                                                                                                                                                                                    PCT-US94-09450-4
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2al Similarity 41, Conser 75 NVEGSY 432 NAKGNYQSI 111 GLYVDEW	Best Local Similarity 22.3%; Pred. No. 0.7; Matches 41; Conservative 32; Mismatches 46; Indels 65; Gaps 13;	75 NVEGSYGVRQSFGKNONPAGWIGNPNHVKYKIEWLN 110	432 : :	111 GLSYVGDFWNRSHLIADSLGGDALRVNAVTGTRTQNV-GGRDQKGGMRYTEORAOEW 166	489 TLGYSDTYSESVYKSHILSEYGFYNQNIYKGRTQRWQLTSSTSLKW 534	167 LEANRDGYLYYEVAPIYNADELIPRAVVVSMOSSDNTINEKVLVYNTANGYTIN 220	535 MDYNFWPAIGIYNSEQRQLTDKGGYISVTITRASRENSIANTGYSYN 580		
	l Similarit 41; Conse	75 NVEGSY	32 NAKGNYQS	11 GLSYVGDF	89 TLGYSDTY	67 LEANRDGY	35 MDYI	21 YHNG 224	1 Vep 504

Search completed: January 5, 2004, 18:44:02 Job time : 27.1473 secs

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January 5, 2004, 18:41:44; Search time 424.262 Seconds (without alignments) 108.298 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                               1220
1 RQTQVSNDVVLNDGASKYLN.....VYNTANGYTINYHNGTPTQK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT7 MWF VUBL.pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT7 MWF VUBL.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:
/cgn2_6/ptodata/2/pubpaa/US10_MEW_PUB.pep:
/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:
/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          733937 segs, 200641211 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 9, Appli	Sequence 8, Appli	Sequence 15, Appl	Sequence 6, Appli	Sequence 16, Appl	Sequence 129, App	Sequence 168, App	Sequence 4, Appli	Sequence 4312, Ap	Sequence 7751, Ap	Sequence 6, Appli	Sequence 354, App	Sequence 8616, Ap	Sequence 1312, Ap	Sequence 20377, A
SUMMARIES		QI	US-09-119-900-9	US-09-119-900-8	US-09-119-900-15	US-09-119-900-6	US-09-119-900-16	US-09-769-736-129	US-09-769-744A-168	US-09-119-900-4	US-09-738-626-4312	US-10-156-761-7751	US-09-839-894-6	US-10-369-493-354	US-10-156-761-8616	US-10-369-493-1312	US-10-369-493-20377
		8	Q	σ	0	σ	o	12	12	σ	10	15	10	12	15	12	12
		Watch Length DB	229	271	272	38	32	261	274	23	1233	2386	867	398	609	422	422
	Query	Match	100.0	100.0	99.6	16.6	13.9	10.7	10.0	8.7	8.7	8.0	7.5	7.4	7.2	7.1	7.1
		Score	1220	1220	1215	202	170	131	122.5	106	106	97	92	90	87.5	87	87
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64466, 104466,	Sequence 394, App Sequence 395, App Sequence 14, Appl Sequence 16599, A Sequence 7, Appli
US-10-28 US-01-28 US-01-28 US-09-815 US-09-815 US-09-740 US-09-740 US-10-36	
112 123 124 125 125 126 127 127 127 127 127 127 127 127 127 127	122
428 228 229 11136 11136 11136 11739 11739 11198 1198 1198 1198 1198 1198 1198 1198 1198 1198 1198 1198 1198 1198 1	1723 1723 479 534 811
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11111232222222222222222222222222222222	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF SEQUENCES: 16
NUMBER OF SEQUENCES: 16
NUMBER OF SEQUENCES: 16
TITLE OF SEQUENCES: 16
TITLE OF SEQUENCES: 16
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TITLE OF SE
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
FILING DATE:
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/082,845
APPLICATION NUMBER: US/08/082,845
FILING DATE:
FATORNEY/AGENT INFORMATION:
NAME: PRIORSY, MICHAEL B.
REGISTRATION NUMBER: 9521
TELECHONE: (818) 795-4000
TELEPHONE: (818) 795-4321
INFORMATION FOR SEQ ID NO: 9:
Sequence 9, Application US/09119900; Patent No. US20020081622A1; GENERAL INFORMATION:
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MOLECULE TYPE: protein
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CITY: Pasadena
STATE: Californ:
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            US-09-119-900-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RQTQVSNDVVLNDGASKYLNBALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 60
                                                                                                                                                                                                                                                                                1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
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                                                                                                                                                                                                    Length 229;
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APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                100.0%; Score 1220; DB 9;
100.0%; Pred. No. 1.1e-117;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTY: USA
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APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                             Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/09119900
Patent No. US20020081622A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Farber, Michael B. REGISTRATION NUMBER: 32,612 REFERENCE/DOCKET NUMBER: 955 TELECOMMUNICATION INFORMATION: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 271 amino acids TYPE: amino acid
    SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 229; Conservative
                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 91001
                                                                                                                                         ORGANISM:
US-09-119-900-9
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US-09-119-900-8
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                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                           Length 271;
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                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant DNase B Derived from Streptococcus pyogenes
; Score 1220; DB 9;
; Pred. No. 1.4e-117;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/09119900
Patent No. US20020081622A1
GENERAL INFORMATION:
APPLICANT: APRLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Streptococcus p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
    Query Match
Best Local Similarity 100.0%;
Matches 229; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-09-119-900-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
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PRIOR APPLICATION NUMBER: GB 9816335.5
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                                                                                                                                                                                                                                                                                      STREET: 225 South I
CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 91001
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ORGANISM:
US-09-119-900-16
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                                                                                    105 GRIRTARGTLIYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNR 164
                                                                                                                                                                    165 SHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAP 224
45 QTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDEL 104
                                                                                                                                            122 SHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAP 181
                                                              62 GRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNR
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                                                                                                                                                                                                                                                   225 IYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROTOVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 202; DB 9; I
Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.6%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B De
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISCHRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPAX: (818) 795-4000
TELEPAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09119900 Patent No. US20020081622A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Pasadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 38; Conserva
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                                         GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Parg, Patty P.-Y.
APPLICANT: Belei, Maxina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Makh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 170; DB 9; I
Pred. No. 1.7e-10;
                                                                                                                                                                                                                                                                          225 South Lake Avenue, Ninth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
13.9%; Score 170; DE
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 32; Conservative 0; Mismatches
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CURRENT FILING DATE: 2003-02-14
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
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                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 129, Application US/09769736 Publication No. US20030138775A1 GENERAL INFORMATION:
Sequence 16, Application US/09119900 Patent No. US20020081622A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE DOCKET NUMBER: 952
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
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198 STGQNYYESKVRKALDQNK-~RVRYRVTLYYASNEDLVPSASQIEAKSSDGELEFNVLVP 255
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                                                                                                                                                                                                                                                                             APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/119,900
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225 South Lake Avenue, Ninth Floor
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
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; Sequence 4312, Application US/09738626
; Sequence 4312, Application US/09738626
; CENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pyogenes
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                                                                                                                                                                                         Sequence 4, Application US/09119900
Patent No. US200200081622A1
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Farber: Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                                            212 NTANGYTINYHNGTPT 227
                                                                                      256 NVQKGLQLDYRTGEVT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (818) 796-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (818) 795-6321
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                               ADDA...
STREET: 225 CITY: Pasadena
CITY: Pasadena
California
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Best Local Similarity
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US-09-119-900-4
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                                                                                                                                                                                                                                                                                                                     89 NONPAGW--TGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGD-----ALRVNA 138
                                                                                                                                                                                                                                                                                                                                                                125 NWKPLGWHQVATNDHYGHAVD------KGHLIAYALAGNFKGWDASVSNPQNV 171
                                                                                                                                                                                                                                                                                                                                                                                                        139 VIGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNAD-ELIPRAVVVSM 197
                                                                                                                                                                                                                                                                                                                                                                                                                                     43 TPALFPKAGDILYSKLDE--LGRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- TPPGW---- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 SQALAESVITDAVKSQIKGSLEWNGSGAFIVNGNKTNLDAKVSSKPYADNKTKTVGKETV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 HVKYKIEWLNGLSYVGDFWNRSHLIADSL----GGDALR---VNAVTGTRTQNVGGRDQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 KGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQSSDNTINEKVLVY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SPNYYKTLGTSQI 42
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                                                                                                                                                                                                                                                                             26;
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10.0%; Score 122.5; DB 12; Length 274;
Best Local Similarity 22.3%; Pred. No. 0.00028;
Matches 57; Conservative 34; Mismatches 100; Indels 65;
                                                                                                                                                                                                                                 10.7%; Score 131; DB 12; Length 261; 26.0%; Pred. No. 3.5e-05; tive 25; Mismatches 60; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 ----PTVANALLSKATRQYKNRKETGNGSTSW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: De Fage, ALCLALLA ...
APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
APPLICANT: Hansbro, Philip M
ITLLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21123NO
CURRENT APPLICATION NUMBER: US/09/769,744A
CURRENT PILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: GE 9816336.3
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 168
LENGTH 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 QSSDNTINEKVLVYNTANGYTINYHNGTPT 227
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               PRIOR APPLICATION NUMBER: US 60/125163
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 168, Application US/09769744A Publication No. US20030134407A1 GENERAL INFORMATION:
                                                                                                                                            TYPE: PRT
ORGANISM: Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-744A-168
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PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                             39; Conservative
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Best Local Similarity
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                                                                                                                                                                                         US-09-769-736-129
                                                                                                                          LENGTH: 261
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1433 TATTNDVQTVLTYGYDNLSRATSVRSGADELAAWVWDDPA---ATGGKGQITSAVSRDAS 1489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 ----TGTRTQNVGGRDQKGGMRYTEQRAQEWL-----EANRDGYLYYEVAPIYNADEL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 RTARGTLTYANVEGSY------GVRQSF------GKNQNPAGWTGNPNHVKYK-- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 ----IEWLNGLSYVGDFWNRS----HLIADSLGGDALRVNAVTGTRTQNV-GGRDQKGG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522 WQLTSSTSLKWMD-----YNFWPAIGIYNSEQRQLTDKGGYISVTLTRASRENSLNA--- 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 MRYTEQRAQEWLEANRDGYLYYEVAPIYNAD--ELIPR----AVVVSMQSSDNTINEKVL 209
                                                                                                                                                                                         3 TQVSNDV--VLNDGASKY-----LNEALAWTFNDSPNYYKTLGTSQITPALFPKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 ITKNISVQQQASVI-----DNKNYYE------GSLKWNSGILSGSL
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                                                                                                                                                                                                                                                                                                                                                                                   106 IEWLNGLSYVG------DFWNRSHLIADSLGGDALRVNAV-----
                                                                                              DB 15; Length 2386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Daily, Myron M.
APPLICANT: Levine, Myron M.
APPLICANT: University of Maryland
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF THE
TITLE OF INVENTION: CSA OPERON
TITLE OF INVENTION: CSA OPERON
TITLE REFERENCE: UOFMD.006A
CURRENT APPLICATION NUMBER: US/09/839,894
CURRENT FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/198,626
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FRAELSEQ for Windows Version 4.0
                                                                                                                                        25; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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20.4%; Pred. No. 2;
tive 43; Mismatches .68;
                                                                                              8.0%; Score 97; DB 1
21.7%; Pred. No. 2.6;
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09839894 Patent No. US20020176868A1 GENERAL INFORMATION:
                                                                                           Query Match 8.0% Best Local Similarity 21.7% Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 20...
Best Local Similarity 20...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Barry, Eileen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Altboum, Zeev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: E. coli
US-09-839-894-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-839-894-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 6
LENGTH: 867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1020 YETEERAIERRNSQSYIREIGGSEL------WNILKGNSEGLSLAQKCAPQATEINVI 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 --EGSYGVRQSFGKNONPAGWTGNPNHVKYKIEWLNG------LSYVGDFWNRSHLI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 ADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLY-----Y 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 EV-API-----YNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 YLNBALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDBLGRTRTARGTLTYANV-
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8.7%; Score 106; DB 10; Length 1233;
Best Local Similarity 22.8%; Pred. No. 0.12;
Matches 55; Conservative 33; Mismatches 93; Indels 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7751, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: SHIRAWA, TADAYOSHI
APPLICANT: SHIRAY, WOSHIYUKI
APPLICANT: HATTORI, WASHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7751
LENGTH: 2386
                                                                                                            APPLICANT: IKEDA, MASATO
PEPLICANT: OZAKI, AKTO
TITLE OR INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                              CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PLICATION NUMBER: JP 00/159162
PRIOR PELING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4312
                                               OKOI, HARUHIKO
HAYASHI, MIKIRO
                                                                  TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1231 † 1231
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Serven C.
APPLICANT: Slater, Serven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                    481 ATTGYEAEAAANTLSGNASVGGCDACSGGKKVGNLYTGGKLRINDITVKKDG--IYTVKV 538
                                                                                                                                                                                                                     382 VIAVDONTSPVARPVTPVGDQQVWGT---KNADGSYTV-ALFNLGDSPASVTAHWASFGF 437
                                                                                                                                                                                                                                                                    --GGDALRVN 137
                                                                                                                                                                                                                                                                                                                                                   138 AVTGTRTQ------NVGGRD----QKGGMRYTEQRAQ-EWLEANRDGYLYYEVAP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 VEGSYGVRQSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVG------DFWNRSHLIA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 YLN-EALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTR-TARGTLTYAN
                                                     Gaps
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                                                 Indels 113;
                                                                                         13 DGASKYLNEA--LAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELG-
           DB 15; Length 608;
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                                                                                                                                                                                                                                                                TGNPNHVKYKIEWLNGLSYVGDFWNRSHL----IADSL--
                                                 60;
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    7.2%; Score 87.5; Di
4.4%; Pred. No. 3.6;
ve 25; Mismatches
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Best Local Similarity 25.9%; Pred. No.
Matches 56; Conservative 30; Mismatc
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Publication No. US20030233675A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 IYNADELIPRAVVVSMQSSDNT 203
    Query Match 7.2%; Sco
Best Local Similarity 24.4%; Pro
Matches 64; Conservative 25;
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US-10-369-493-1312
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US-10-369-493-20377
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                                                                                                                         APPLICANT: Cap. Yongwei

APPLICANT: Cap. Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Ghan, Warry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NOS: 47374
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1. Similarity 24.6%; Pred. No. 1.1;
31; Conservative 18; Mismatches 43
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APPLICANT: SHEA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 299-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-06-02
PRIOR PILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SQ ID NO 8616
LENGTH: 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8616, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRGANISM: Streptomyces avermitilis US-10-156-761-8616
                      ||: || |
-----GYSYNYSRG 582
210 VYNTANGYTINYHNG 224
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 31; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 ANGYTI 219
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US-10-369-493-354
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APPLICANT: Cao. Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Stewen C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
FRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20377
TYPE: LENGTH: 422
TYPE: ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 DSLGG----DALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 YLN-EALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTR-TARGTLTYAN 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.1%; Score 87; DB 12; Length 422; Best Local Similarity 25.9%; Pred. No. 2.4; Matches 56; Conservative 30; Mismatches 72; Indels
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Search completed: January 5, 2004, 19:13:47 Job time : 425.262 secs

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OM protein - protein search, using sw model

Run on:

January 5, 2004, 17:31:14 ; Search time 26.5691 Seconds (without alignments) 828.882 Million cell updates/sec

US-08-482-785-9 1220 1 RQTQVSNDVVLNDGASKYLN.......VYNTANGYTINYHNGTPTQK 229 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mitogenic factor,	deoxyribonuclease	hypothetical prote	DNA-entry nuclease	endA protein - Str	deoxyribonuclease	probable outer mem	alpha-toxin precur	cfaC protein precu	P-glycoprotein - T	conserved hypothet	pullulanase - Ther	botulinum neurotox	Alpha-Hemolysin pr	uncharaterized con	hypothetical prote	hypothetical prote	autolysin (amidase	penicillin amidase	glutamate dehydrog	probable glutamate	hyaluronate lyase	hypothetical prote		alpha-qalactosidas	hypothetical prote		w	gtfB protein precu
SUMMARIES	ΩΙ	836907	JT0584	D86644	F95229	S10641	A99094	G71896	869209	C56617	T30295	AB1481	S27545	S58857	F89887	F97223	E84483	876412	AG1565	139665	JN0854	A71038	E90016	S76211	S41915	JC5558	B70333	\$59951	H89821	B33135
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	Length	271	327	263	274	274	274	455	319	869	1534	386	1203	292	319	347	928	4199	774	802	420	422	803	611	1116	396	729	1182	1183	1475
de	Query	99.7	٩.	12.6	ö	10.0	ö	9.6	•	•	•	7.5	٠	7.4	•	7.3	7.3	7.3	7.2		7.1	7.1	7.1			7.0		7.0	•	7.0
	Score	1216	365	153.5	122.5	122.5	122.5	104.5	94	91.5	91.5	91	91	90.5	90	89.5	83	83	88	88	87	87	B	86.5		96	98	98	98	85.5
	Regult No.	7	8	m	4	ហ	9	7	80	თ	10	1	12	13	14	15	16	17	18	19	70	21	22	23	24	25	56	27	28	29

probable peptidogl	outer membrane pro	outer membrane pro	glutamate dehydrog	probable outer mem	starch-degrading e	probable ABC trans	probable DNA-direc	prophage pi3 prote	botulinum neurotox	outer membrane por	maltose/maltodextr	hypothetical prote	hypothetical prote	DNA-directed RNA p	conserved hypothet
AB1180	D90755	B85619	D75176	H71942	S31940	C84423	T38867	D86798	H44644	MMECF	G70033	A98014	C85858	877518	AG1120
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2044	362	362	420	479	503	725	1165	1640	293	362	417	836	836	1102	386
7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.9	6.8
35.5	82	82	82	82	85	82	82	82	84	84	84	84	84	84	83.5
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ALIGNMENTS

yogenes gene e

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8; PID:9432370

Y.; Igarashi,

RESULT 1		
mirodenic	factor	25K. preciirsor - Strentococcus pyogenes
C; Species:	s: Streptoco	6.74
C;Date:	10-Dec-1993	C;Date: 10-Dec-1993 #Bequence_revision 23-Feb-1996 #text_change 15-Oct-1999
C;Access	ion: 836907	529188
R; Iwasak	R;Iwasaki, M.; Igarashi, H.; I FEBS Lett 331 187-192 1993	ashi, H.; Hinuma, Y.; Yutsudo, T. -192 1993
A;Title:	Cloning, cl	. ILL Bett: 521, 10, 171, 173, 1735 A;Title: Cloning, characterization and overexpression of a Streptococcus p
A, Refere	A; Reference number:	36; PMID:8405402
A, Access	A, Accession: S36907	
A; Molecule t	A; Molecule type: DNA	
A; Kesidu	A;Kesiaues: 1-2/1 <1WA> A:Cross-references: FMB	LWA> EMBL: D13428: NTD: 0432369: PTDN: BAA02693 1: PTD: 01003196
A, Access	ion: \$36908	11.500 post 10.000 post 10.000 post 11.000
A, Molecu	A, Molecule type: protein	otein
A, Residu	A; Residues: 44-64 < IWW>	
R; Yutsudo,	o, T.; Murai, H.;	i, H.; Gonzalez, J.; Takao, T.; Shimonishi, Y.; Takeda,
A.Title.	A new type	of mitogenic factor produced by Streptococcus pyogenes
A, Refere	A;Reference number: S29188;	MUID:92354761; PMID:1644200
A; Access	A; Accession: S29188	
A;Molecu		otein
F:1-43/Domai	es: 44-64 <rur></rur>	A;Kesiques: 44-64 P:1-43/Domain: gignal gemience #status predicted <sig></sig>
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Query Match	Match	
Best L	cal Simi	99.6%; Pred. No. 4.3e-96;
Matches	228;	Conservative 0; Mismatches 1; Indels 0; Gaps
δ	1 ROTOV	ROTOVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
ορ	43 RQTQV	ROTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
δ	61 LGRTR	LGRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKI EMLNGLSYVGDFWN
DÞ	 103 LGRTR1	LGRITRIARGILIYANVEGSYGVROSFGRONDPAGWIGNPNHVKYKIEWLNGLSYVGDFWN
•		
ò	121 RSHLI	RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA
οp	163 RSHLI	RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEAA
δλ	181 PIYNAL	PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTOK 229
Dp	223 PIYNAL	PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 271

ö

120 162 180 222

102

9

RESULT 2 710584 deoxyribonuclease I (BC 3.1.21.1) sdc precursor - Streptococcus "equisimilis" NyAlternate names: streptodornase

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C;Species: Streptococcus pneumoniae
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Oct-1999
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Oct-1999
C;Date: 10-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Oct-1999
R;Poyet, A.; Greenberg, B.; Lacks, S.A.
J; Mol. Biol. 213, 727-738, 1990
A;Title: Genetic and structural characterization of enda. A membrane-bound nuclease requires greened and structural characterization of A;Title: Genetic and structural characterization of A;Title: Genetic and structural characterization of A;Title: Genetic and structural characterization of A;Title: Genetic and structural characterization of A;Title: Genetic and Structural characterization of A;Title: Genetic and Structural characterization of A;Title: Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Structural characterization of Genetic and Genetic and Genetic and Genetic and 
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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: F95229
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005672; PIDN:AAK76031.1; PID:g14973470; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HVKYKIEWINGLSYVGDFWNRSHLIADSL----GGDALR---VNAVTGTRTQNVGGRDQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---HQVKNLKG-SYTHAV-DRGHLLGYALIGGLDGFDASTSNPKNIAVQTAWANQAQAEY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQSSDNTINEKVLVY 211
                                                                                                                                                                                                                                                                   219
                                         --NAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42
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                                                                                                             136 SGINNEARNLVPETAMFNGGNFTGTNDGNT-----ASMLYYENRLDSWLANHPNYYLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-entry nuclease [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
10.0%; Score 122.5; DB 2;
Best Local Similarity 22.3%; Pred. No. 0.0056;
Matches 57; Conservative 34; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PTVANALLSKATRQYKNRKETGNGSTSW-----
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                                                                                                                                                                                                                          178 EVAPIYNADELIPRAV----VVSMOSSDNTINEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endA protein - Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 NVQKGLQLDYRTGEVT 271
                                                                                                                                                                                                                                                                                                                                                                                                       220 NYHNGT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 NYADGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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C; Species: Streptococcus "equisimilis"
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 15-Oct-1999
C; Accession: JT0584; S24204
R; Wollnowska, R:, Ceglowski, P:; Kok, J:; Venema, G.
R; Wollnowska, R:, Ceglowski, P:; Kok, J:; Venema, G.
Gene 106, 115-119, 1991
A; Title: Isolation, sequence and expression in Escherichia coli, Bacillus subtilis and I.
A; Accession: JT0584
A; Accession: JT0584
A; Molecule type: DNA
A; Residues: 1.327 «WOL»
A; Residues: 1.327 «WOL»
A; Experimental source: ERBL:X17241; NID:948693; PIDN:CAA35106.1; PID:948694
A; Experimental source: strain H46A
C; Genetics:
A; Experimental source: strain H46A
C; Genetics:
A; Experimental source: strain H46A
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Biblotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: D86644

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein ybfB [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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A,Residues: 1-263 <STO>
A,Residues: 1-263 <STO>
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A,Experimental source: strain IL1403
C,Genetics:
A,Gene: ybfB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NPVGW----H-NYNFYYKKSDGSIGKMWLMARGHLVGYQF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 VPVVLTTLKGKKYNSHLFVASHLFADSLGGKSIRKNAITGTQMQNVGTR--KGGMQYIEK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINY 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 KVLSHITKNPDDVYVFYSAIPEYQGAELLARSVLVSALSSDGVINETVRVENTADGENINY 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 TYGEYKDYYTVIGESNIDQSAFPKIYKTTERVYKGQGTSEKRVTVSDVVYNPLDGYKRST 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDNSSQVSTKSLASSVKQAPLTFKNQRQMVMANTDALGRAVDSHIQLKDSQEPKVKREPL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 327;
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12.6%; Score 153.5; DB 2;
Best Local Similarity 24.4%; Pred. No. 1.2e-05;
Matches 60; Conservative 26; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFNDSPNYYKTLGTS-QITPALFPKAGDILYSKLDELGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 29.9%; Score 365; DB 2; L Similarity 34.6%; Pred. No. 1.6e-23; 84; Conservative 34; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 TENDSPNYYKTLGTSQITPALFPK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TARGILIYANVEGSYGVRQSFGKNONPAGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 EKG 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56
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probable outer membrane protein - Helicobacter pylori (strain J99)
C.Species: Helicobacter pylori
A;Variety: strain J99
C.Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 26-May-2000
C;Accession: G71899
E.Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: G71896
A;Accession: G71896
A;Accession: G71896
A;Accession: G71896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:AE001439; NID:g4155275; PIDN:AAD06302.1; PID:g415528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVROSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNAVT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AITADAVS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 GTRTQNVGGRDQKGGM-----RYT-EQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 VEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWL-NGLSYVGDFWNRSHL-----IA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-toxin precursor - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 06-Sep-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C;Accession: S69209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 DSPNYYKTLGTSQITP--ALFPKAGDILY-----SKLDELGRTRTARGTLTYANVEGSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 G---rvfgggvyrgflwgilgrytyatrasersinlnlgykwgsfarv-
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19.3%; Pred. No. 1.8;
ve 42; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Superfamily: Helicobacter pylori hypothetical protein HP0209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 GYYQNFGNANARIGWYGNPIPPNYR----NNSVYGGVFSN----
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F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-319/Product: alpha-toxin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.6%; Score 104.5; DB 2;
25.2%; Pred. No. 0.37;
tive 19; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hedengrahn, G.
submitted to the EMBL Data Library, October 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 VSMQSSDNTINEKVLVYNTANGYTINYHNG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 DSPNYYKTLGTSQITPALFPKAGD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GB:AE001503; A,Experimental source: strain J99
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Best Local Similarity 25.2%;
Matches 53; Conservative
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nes 47; Conserv
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A;Molecule type: DNA
A;Residues: 1-319 <HED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-455 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Genetics:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               decyylbonuclease I (EC 3.1.30.-) [imported] - Streptococcus pneumoniae (strain R6) C;Species: Streptococcus pneumoniae (species: Streptococcus pneumoniae (space: 22-0ct-2001 #sequence_revision 22-0ct-2001 #sequence_revision 22-0ct-2001 #sequence_revision 22-0ct-2001 #sequence_revision 22-0ct-2001 #sequence_revision 22-0ct-2001 C;Accession: A99094 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F. R;Hoskins, D.J.; Leslanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N.; B.; Sun, P.M.; Winkler, M.S. 2001 A; Sun, J.; Matsushima, P.; McAhren, S.; N.; Althors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Reference number: A97872; MulD:21429245; PMID:11544234
                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STGQNYYESKVRKALDQNK--RVRYRVTLYYASNEDLVPSASQIEAKSSDGELEFNVLVP 255
                                                                                                                                                                                                                                                                                                             50 SQALAESVLTDAVKSQIKGSLEWNGSGAFIVNGNKTNLDAKVSSKPYADNKTKTVGKETV 109
                                                                                                                                                                                                                                                                                                                                                                          43 TPALFPKAGDILYSKLDE--LGRTRTARGTLTYANVEGSYGVRQSFGKNONPAGWTGNPN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- TPPGW---- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 HVKYKIEWLNGLSYVGDFWNRSHLIADSL----GGDALR---VNAVTGTRTQNVGGRDQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 KGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQSSDNTINEKVLVY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 TPALFPKAGDILYSKLDE--LGRIRTARGILTYANVEGSYGVRQSFGKNOMPAGWTGNPN 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: AE007317; PIDN: AAL00582.1; PID: g15459463; GSPDB: GN00174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 HVKYKIEWLNGLSYVGDFWNRSHLIADSL----GGDALR---VNAVTGTRTQNVGGRDQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 KGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQSSDNTINEKVLVY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TQVSNDVVLNDGASKYLNEALAWTFND------SPNYYKTLGTSQI 42
                                                                                                                                                                                              Gaps
A,Molecule type: DNA
A,Residues: 1-274 <PUY>
A,Cross-references: GB:X54225; NID:g47372; PIDN:CAA38134.1; PID:g47374
                                                                                                                                                                                        65;
                                                                                                                               DB 2; Length 274;
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                                                                                                                        Query Match 10.0%; Score 122.5; DB 2; Length 3 Best Local Similarity 22.3%; Pred. No. 0.0056; Matches 57; Conservative 34; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PTVANALLSKATRQYKNRKETGNGSTSW----
                                                                                                                                                                                                                                                    3 TQVSNDVVLNDGASKYLNEALAWTFND----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 NTANGYTINYHNGTPT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 NVQKGLQLDYRTGEVT 271
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                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Status: preliminary
A Molecule type: DNA
A, Residues: 1-274 <KUR>
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101

Gaps

161

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Riclaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H., Science 294, 849-852, 2001.

Science 294, 849-852, 2001.

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matl ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein, probable lipoprotein lin0385 [imported] - Listeria innocu
                                                                                                                                                                                                                                                                                                                                                 1224 DEL-RRITRRAADVIATVPGEASAR---SKGOHPETTAGWLEFREVEMRYRAGLPLVLDR 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 --KGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNAD----ELIPRAVVVSMQSSDNTINE 206
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A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R-----AQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSS--DNTINE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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C;Genetics:
A;Note: TCPGP2
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding
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                                                                                                                                   Length 1534;
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pullulanase - Thermoanaerobacterium thermosulfurigenes
C;Species: Thermoanaerobacterium thermosulfurigenes
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                                                                                                                                                                                                                                                                                     59 DELGRIRIARGILIYANVEGSYGVROSFGKNONP---AGW
                                                                                                                                      DB 2;
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                                                                                                                                   7.5%; Score 91.5; E
25.4%; Pred. No. 23;
tive 23; Mismatches
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                                                                                                                Query Match
Best Local Similarity 25.4%
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A Molecule type: DNA
A, Residues: 1-386 <GLA>
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Best Local Simi
Matches 55;
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C;Species: Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000
C;Accession: T30295
R;Dallagiovanna, B.; Gamarro, F.; Castanys, S.
Mol. Biochem. Parsaitol. 75, 145-157, 1996
A;Title: Molecular characterization of a P-glycoprotein-related tcpgp2 gene in Trypanosoc
A;Title: Molecular characterization of a P-glycoprotein-related tcpgp2 gene in Trypanosoc
A;Title: Molecular characterization of a P-glycoprotein-related tcpgp2 gene in Trypanosoc
A;Reference number: Z11742; MUID:96258555; PMID:8992313
A;Accession: T30295
A;Molecule type: DNA
A;Residues: 1-1534 *DNA
A;Residues: 1-1534 *DNA
A;Cross-references: EMBL:Z49222; NID:g1150649; PIDN:CAA89197.1
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C; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 08-Oct-1999
C; Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 08-Oct-1999
C; Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 08-Oct-1999
C; Jan-1996 #sequence of region 1 of the CFA/I fimbrial operval; Thitle: The complete nucleotide sequence of region 1 of the CFA/I fimbrial operval; The ference number: A56617; MUID:92329981; PMID:1352712
A; Reference preliminary
A; Residues: 1-869 < AOR>
A; Residues: 1-869 < AOR>
A; Residues: 1-869 < AOR>
A; Cross-references: GB:M55661; NID:9145507; PIDN:AAC41416.1; PID:9145510
A; Experimental source: enterotoxigenic strain, CFA/I-ST plasmid NTP113
A; Mote: sequence extracted from NCBI backbone (NCBIN:108960, NCBIP:108971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             488
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                                                                                                                                                         159 TEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYT 218
       : | | | | :: | :: | :: | :: | : : | :: | :: | :: | :: | :: | : : | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
                                                                                                            -- RDOKGGMR--Y 158
                                                                                                                                                                                                                                                                                                           198 NNMVNQNWGPYDRDSW-----NPVY-GNQLFMKTRNGSMKAADNFLDPNKASSLLSSGFS 251
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                                                                                                                    DSLGGDALRVNAVTGTRTQNVGG---
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Best Local Similarity
Matches 41; Conserv
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A;Genome: plasmid
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Alpha-Hemolysin precursor [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 01-Mar-2002
C;Accesion: F89887
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: GB:BA000018; PID:g13700962; PIDN:BAB42258.1; GSPDB:GN00149
A,Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 VEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWL-NGLSYVGDFWNRSHL------IA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RDQKGGMR--Y 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 TEQRAGEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 YGFNGN-----VTGDDTGKIGGLIGANVSIGHTLKYVQPDFKTILESPTDKKVGWKVIF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 NNMVNQNWGPYDRDSW-----NPVY-GNQLFMKTRNGSMKAAENFLDPNKASSLLSSGFS 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE001437; PIDN:AAK80577.1; PID:g15025656; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---ILYSKLDELGRTRTARGTLTYAN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 DSDINIKT-GTTDIGSNTTVKTGDLVTYDKENGMHKKVFYSFIDDKNHNKKLLVIRTKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.3%; Score 89.5; DB 2; Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 DSLGGDALRVNAVTGTRTQNVGG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                         260 ALD----LYNSQTANGTTIQVFNYH-GDDNQK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 DSPNYYKTLGTSQITPALFPKAGD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Mismatches
            203 TINEKVLVYN--TANGYTI---NYHNGTPTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4%; Score 90;
8.9%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Superfamily: leukocidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Residues: 1-319 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: F89887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: SA1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Genetics:
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                                                                                                                                      RESULT 14
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C;Date: 09-Jun-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C;Accession: $27545
R;Burchhardt, G; Hackel, K.; Spreinat, A.; Antranikian, G.; Bahl, H.
Bubmitted to the EMBL Date Library, March 1992
A;Description: Nucleotide sequence of the pullulanase gene from Clostridium thermosulfur A;Reference number: $27544
A;Accession: $27545
A;Stelminary
A;Stelminary
A;Molecule type: DNA
A;Residues: 1-1203 <BUR.
A;Residues: 1-1203 <BUR.
A;Note: the source is given as Clostridium thermosulfurogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
$58857
botulinum neurotoxin type B hemagglutinin component, 33K - Clostridium botulinum (strain botulinum neurotoxin type B hemagglutinin component, 33K - Clostridium botulinum (strain NALcernate names: protein HA-33
C;Species: Clostridium botulinum A;Variety: strain Eklund 17B
C;Accession: 558857
B;East, A.K.; Stacey, J.M.; Collins, M.D.
Syst. Appl. Microbiol. 17, 306-312, 1994
A;Title: Cloning and sequencing of a hemagglutinin component of the botulinum neurotoxin A;Reference number: SS8855
A;Accession: SS8855
A;Accession: SS8855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1034 HIIGVDKPTEDIYAEVWADGLTNSTGQGPNMIAQLGYKYV-----SGTVYDSVYGSV-- 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1086 YNSVYGVDDSGFTWVNAQYVGDIGNNDQYKASFTPDKIGQWEYLMRFSDNQGQDWITTST 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 ----DILY--SKLDELGRIRTARGTLIYANVEGSYGVRQSFGKNONPAGWIGN-----PN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 HV------KYKIEWLNGLS-------YVGDFWNRSHLIADSLGGDALR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 ANVEGSYG-VRQSFGKNQNPAGWTGNPNHVKY-----KIEWLNGLSY-----V 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 SDFNNFTCKISPILDSSKVVQQVAMTDLSVNLYTWDY-----GRNQKWTIKYNKEKSAYQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 FFNTILSNGVLTWISSNGNTVRVSSIAQNNDAQYWLINPVSNAYETY---TITNLHDTTK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   931 QAPSINVVVTSGNGKV---DLSWLQSDGATGYNIYRSSVEGGLYEKIASNVTETTFEDANV 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KGG-----MRYTEQRAQEWLEANR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 SNADNQYWLLLKDIGSNSFIIASYKNPNLVLYADTVARNLKLSTLNNSSYIKFIIEDYMI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 GDFWN------RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQ-- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EWLEAN-----RDGYLYYEVAPIYNADELIPRAVVVSMQSSDN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                    4 QVSNDVVLNDGASKYLNEALAWIFNDSPNYYKTLGT------SQITPALFPKAG- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: DNA
A;Residues: 1-292 <EAS>
A;Cross-references: EMBL:X79103; NID:g870932; PIDN:CAA55714.1; PID:g870935
A;Experimental source: strain Eklund 17B
C;Keywords: hemagglutinin; neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | | : | | : | | 1146 ---ESFYVVP---SDDLIKPTAPYLNQPGTES--SRVSLTWNPSTDNVGNY 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 DGYLYYEVAPIYNADELI-PRAVVVSMQSSDNTINEKVLVYNTANGYTINY 221
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                                                                                                                                                                                                                                                                                                                                  7.5%; Score 91; DB 2; Length 1203; ilarity 21.6%; Pred. No. 19; Conservative 36; Mismatches 86; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 VNAVTGTRTQ-------NVGGRDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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nes 48; Conserva
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                 63;
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Best Local S
Matches 63
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Best Local S:
Matches 48
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12;	29	87	113	141	156	201	216	253			
61; Gaps	LYSKLD	LOESSK	WLNGLS	YAAQIG	DOKGGM	DNSNWS	YNTANG	KNGKNT			
	KAGDI	KIQSI	KYKIE	KIG	NVGGR	IVYPQ	EKVLV 	EPYLI			
Indels	SQITPALFP	KIQSILQESSK	VHNG	TIIKDPNRV	DALRVNAV-TGTRTQNVGGRD	TGFIMSNG	MOSSDNTIN	REAVIT			
100;	KTLGI		SWTGN-	- FTANV	RVNAV-	SVGAIF	RAVVVS	I58			
Best Local Similarity 22.5%; Pred. No. 4.9; Matches 56; Conservative 32; Mismatches 100; Indels	3 TQVSNDVVLINDGASKYLNBALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLD 59	49 TNVRNTIISTLMGTGAHKYMAKWFFSDA	60 BLGRIRTARGILIYANVEGSYGVRQSFGKNQNPAGWIGNPNHVKYKIEWLNGLS 113	88 SEATTKOSKNDVIKINTDSDITRMQVDGDGKFTANVLIIKDPNRVKIGYAAQIG 141	114 YVGDFWNRSHLIADSLGGDALRVNAV-TGTRTQNVGGRDQKGGM 156	142 YVGETTREMAKRYKAVAAINGGYFKDTSPNKQSGGVGAIPTGFIMSNGQIVYPQDNSNWS 201	157 RYTEQRAQEMLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLVXNTANG 216	202 EITSEENRALTIDKDGNLQVGGTYSPDQLIKSGIREAVITEPYLIKNGKNT 253			
22.5%; P rative 32;	LNDGASKYLN	FLMGTGAHKYMA	STLTYANVEGSY	NDVIKINTOSDI	WNRSHLIADSLG	AKRYKAVAAING	WLEANRDGYLYY	ALTIDKOGNL	225	262	
imilarity ; Conserv	TOVSNDVV-	TNVRNTIIST	ELGRTRTARC	SEATTKOSK	YVGDFV	YVGETTREM	RYTEORAGE	EITSEEENR	217 YTINYHNGT 225	254 IQANSVSGT 262	
ocal 9	٣	49	9	88	114	142	157	202	217	254	
Best Lo Matches	λ̈́ο	QQ	ò	qa	ò	рр	γo	qq	ò	qa	

Search completed: January 5, 2004, 18:42:52 Job time : 27.5691 secs

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January 5, 2004, 15:46:12; Search time 19.3996 Seconds (without alignments) 555.120 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Run on:

US-08-482-785-9 1220 1 RQTQVSNDVVLNDGASKYLN......VYNTANGYTINYHNGTPTQK 229 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES		
Result No.	0	uer atc	Lengt	DB	ΩI	escr	
-	365	29.9	327	-	DRN1 STREQ		streptococc
7	122.5	10.0	274	Н	NUCE_STRPN	003158 strep	streptococc
n		•	1279	Н	APU THESA		amylopull
4	97	8.0	. 1861	Н	APU_THETU		amylopull
ហ	94	•	319	Н	HLA STAAU		staphylococ
9	91.5	7.5	869	ч	CFAC ECOLI		escherichia
7	90	7.4	341	-	OMPL_PHOPR		photobacter
8	•	7.3	1476		GTFB_STRMU	P08987 strep	streptococc
σ	88.5	7.3	2208		POLN MANCV	_	manchester
10	88	7.2	802		PAC ARTVI	P31956 arthr	arthrobacte
11	87.5		1047	ч	POL_SIVA1		simian immu
12	87		420	-	DHE3 PYRFU		pyrococcus
13	æ	7.1	420	-	DHE3 PYRHO	052310 pyroc	ругососсив
14	•	•	1116	Н	RPOB_HETCA	_	heterosigma
15	ø	•	1709	ч	CHD1_HUMAN	_	homo sapien
16	96	•	296	ч	NIFD_NOSCO		nostoc comm
17	96	•	1182	-	RPOB_STAAU		staphylococ
18	82	٠	420	Ä			pyrococcus
19	82	•	1165	-			schizosacch
20	84	•	362	ч		-	escherichia
21	æ	•	1102	ч	RPOB_SYNY3		synechocyst
22	83.5	6.8	3093	-	POLG BSTV1		od emoi
23	83	6.8	227	ч	XYN1_HUMIN		
24	83	6.8	398	ч	KBL_ECOLI	-	escherichia
25	83	٠	398	7	KBL SALTY	P37419 Balmo	salmonella
56	82.5	٠	480	-	NIFD CYAAS	O07642 cyano	cyanothece
27	82.5	•	1711	7	CHD1 MOUSE	P40201 mus m	mus musculu
28	8		392	Н	PRID_STRGR	P52321 Btrep	streptomyce
58	81.5	•	1723	-	1 - 1	_	ydia p
30	81	9.9	420	-		Q47951 pyroc	pyrococcus
31	81	•	638	П	YQGS_BACSU	P54496 bacillus	lus su
32	81	9.9	999	-	11	P39046 enter	enterococcu
33	81	9.9	1196	ч	AMYB_PAEPO	21543	paenibacill

P16154 clostridium Q92e31 rickettsia	Q89853 ebola virus P27034 agrobacteri P50900 clostridium	P19424 bacillus sp Q56110 salmonella	P04063 hordeum vul P93119 daucus caro	Q929m2 bacillus ha Q9rlt9 listeria mo	Q00239 plectonema
TOXA CLODI RNC RICPR	VGP_EBORS BGLS AGRTU GUX2_CLOSR	GUN BACS6 OMS1_SALTI	AMY2_HORVU TOP1_DAUCA	RPOB_BACHD RPOB_LISMO	NIFD_PLEBO
77					-
2710	677 818 914	941 394	427 790	1180	494
9.9	6.6 6.6 6.6	9.9 9.9	9.9	9.9	6.5
81 80.5	80.5 80.5	80.5	0 8 8 8	088	79.5
34	36 37 38	39 40 9	4 4 2 7	4 4 4	45

ALIGNMENTS

DRN1 S	3 1	PRT;	327 AA.				
AC							
F F	01-MAY-1992 (Rel. 22, Created) 01-MAY-1992 (Rel 22, Last sec) 11910	ed) gemience undate)				
占	(Rel. 36, Last	notatio	n update)				
DE	xyribonuclease precursor	EC 3.1.	(EC 3.1.21.1) (Streptodornase)	todornase)	(DNase)		
N C							
S C	Streptococcus equisimilis.						
2 6	Bacteria, Firmicutes; Lactobaciliales;	cillale	s; streptococcaceae	ccaceae;			
y :	Streptococcus.						
žč	NCB1_TaxiD=119602;						
3 5							
א ה ה	SECUENCE FROM N.A.						
ָ בְּיִר	SIKAIN=H40A;						
χ ή 2 ή	MEDLINESYZUSYUSI; PUDMEGSIYS/USZ;	1227	omorrow.				
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1 E	Jequence and	ia of t	lactic of the Dasse		577770		
E.	۱ .	e from	dene from Streptococcus equisimilis H46A.	s equisimil	is H46A	=	
넔				•			
႘	-!- FUNCTION: MAY HAVE A ROLE IN S.EQUISIMILIS VIRULENCE	IN S.E	QUISIMILIS V	IRULENCE.			
ပ္ပ	-!- CATALYTIC ACTIVITY: Endonu	ucleoly	tic cleavage	to 5'-			
ပ္ပ	phosphodinucleotide and 5'-phosphooligonucleotide end-products	-phosp	hooligonucle	otide end-p	roducts		
អ							1
ខ្ព	This SWISS-PROT entry is copyright.	right.	It is produced through a collaboration	ed through	a colla	borati	ion
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ខ្ព	the European Bioinformatics Institute.	nstitut	The	are no restrictions	rictions	on i	its
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ဥ	modified and this statement is not removed.	s not r	emoved. Usa	ge by and	for co	mmerci	ial ,
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ည (or send an email to licensegisb-sib.ch).	8D-81D.	cn).				
5							!
DE I	EMBL; X17241; CAA35106.1;						
E E	PIR; JT0584; JT0584.		•				
X.	Hydrolase; Endonuclease; Nuclease;		Signal.				
H	SIGNAL 1 24 C	OR 35 ((POTENTIAL).				
10	25 327	CECAYRI	DECAYKIBONUCLEASE.	, , ,			
ğ	SEQUENCE 327 AA; 36844 MW;	75297	7529702FDF8E4AF7	CKC64;			
g	/ Match 29.9%;	Score 365;	65; DB 1;	Length 327;			
M D	Similality 34.0%; 84; Conservative 34		Mismatches 79;	Indels	46; Gaps	Вď	4
ò	26 TFNDSPNYYKTLGTSQITPALFPK	LPPK		AGDILYSKLDELGRTR	SKLDELG	RTR 65	
		=		=	=		
d d	43 TYGEYKDYYTVIGESNIDQSAFPKIYKTTERVYKGQGTSEKRVTVSDVVYNPLDGYKRST	AFPKIYK	TTERVYKGQGTS	EKRVTVSDVVY	NPLDGYK	RST 102	22
à	66 TARGTLTYANVEGSYGVROSFGKNONPAGWTGNT	FGKNONP	AGWTGN		ij	-PNH 101	1
QQ	: :	: WETNPEP	: SGWFRFYNRADN	EEISEKEYDSR	RTKSYKV	: INN 162	22
į	OBTVERDATION NOT SYNCHOLOGICAL TARGET BANKS THROUGH TAYANT CO.	SULTABO	TANAMA TAGOOT	uaconnomano uaconnomano	AdMiciary	161	
⋩							1
g	163 VPVVLTTLKGKKYNSHLFVASHLFADSLGGKSIRKNAITGTQMQNVGTRKGGMQYIEK	SHLFADS	LGGKSIRKNAIT	GTQMQNVGTR-	- KGGMQY	IEK 220	ö

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RAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=470;
MEDLINE=90294291; PubMed=2359120;
MEDLINE=90294291; PubMed=2359120;
MEDLINE=90294291; PubMed=2359120;
"Genetic and structural characterization of endA. A membrane-bound nuclease required for transformation of Streptococcus pneumoniae.";
0. Mol. Biol. 213:727-738(1990).
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-!- FUNCTION: By degrading DNA that enters the cell, plays a role the competence of cells to be transformed.
-!- SUBCELLULAR LOCATION: Membrane-bound.
-!- SIMILARITY: Belongs to the DNA/RNA non-specific endonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENGENCE FROM N. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 A. 1900 
                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
DNA-entry nuclease (Competence-specific nuclease) (EC 3.1.30.-).
ENDA OR SP1964 OR SPR1779.
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Genome of the bacterium Streptococcus pneumoniae strain R6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                  274 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 293:498-506(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                               43 TPALFPKAGDILYSKLDE--LGRTRTARGTLTYANVEGSYGVROSFGKNONPAGWTGNPN 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 KGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMOSSDNTINEKVLVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=B6A-RI;
MEDLINE=94161255; PubMed=8117096;
Ramesh M.V., Podkovyrov S.M., Lowe S.E., Zeikus J.G.;
Ramesh M.V., Podkovyrov S.M., Lowe S.E., Zeikus J.G.;
"Cloning and sequencing of the Thermoanserobacterium saccharolyticum
B6A-RI apu gene and purification and characterization of the
amylopullulanase from Escherichia coll.";
Appl. Environ. Microbiol. 60:94-101(1994).

[12]
IDENTIFICATION OF PROBABLE VECTOR CONTAMINATION.
                                                                                                                                                                                                                                                                                                                                                                   ----SPNYYKTLGTSQI
                                                                                                                                                                                                                                                                                                                                     65; Gaps
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28-FEB-2003 (Rel. 41, Last annotation update)
Amylogullulanase precursor (Alpha-amylase/Fullulanase) [Includes: Alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucan glucanohydrolase) (Alpha-dextrin endo-1,6-alpha-glucosidase)].
                                                                                                                                                            InterPro; IPR001604; Endonuclease.
Pfam; PF01223; Endonuclease; NUCLEASE NON SPEC; 1.
Competence; Hydrolase; Nuclease; Endonuclease; Signal-anchor;
                                                                                                                                                                                                                                                                                                         DB 1; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermoanaerobacter saccharolyticum.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacterium.
                                                                                                                                                                                                                                                                                                     10.0%; Score 122.5; DB 1; Length 22.3%; Pred. No. 0.0011; tive 34; Mismatches 100; Indels
                                                                                                                                                                                                                                      8 25 SIGNAL-ANCHOR (POTENTIAL).
160 160 BY SIMILARITY.
274 AA, 29890 MW; 59B2243F0150CD98 CRC64;
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 entities requires a license agreement ( or send an email to license@isb-sib.ch)
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                                                                  AE007486; AAK76031.1; -. AE008543; AAL00582.1; -.
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                                                   EMBL; X54225; CAA38134.1; -.
                                                                                                                                                                                                                                                                                                                        Similarity 22.33
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                                                                                                PIR; A99094; A99094.
PIR; F95229; F95229.
PIR; S10641; S10641.
TIGR; SP1964; -.
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                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                             CATALYTIC ACTIVITY: Hydrolysis of (1-6) -alpha-D-glucosidic linkages in pullulan and in amylopectin and glycogen, and the alpha- and beta-limit dextrins of amylopectin and glycogen. SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE PAMILY. SO GLYCOSYL HYDROLASES, ALSO SIMILARITY: Conteains 2 fibronectin type III domains. CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN BY THE PRESENCE OF AN EXTRA C-TERMINAL SEGMENT OF 9 RESIDUES THAT SEEMS TO ORIGINATE FROM A PUC-TYPE VECTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVPSNVVATSGNGKV---DLSWSQSDGATGY-NIYRSSVEGGLYEKIASNVTGTTFEDTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Indels 123;
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.2%; Score 99.5; DB 1; Length 1279;
22.6%; Pred. No. 0.88;
tive 33; Mismatches 80; Indels 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          735 735 BX SIMILLARALI..
1279 AA; 142430 MW; 095CCBCA391624DD CRC64;
                  linkages in oligosaccharides and polysaccharides.
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
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BY SIMILARITY.
BY SIMILARITY.
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InterPro; IPR00648; Alpha_amyl_C.
InterPro; IPR00649; Alpha_amyl_Cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR00189; KN III.
InterPro; IPR00189; Alpha_amylase, IPRam; PF001289; Alpha-amylase_C; IPRam; PF00043; Alpha-amylase_C; IPRam; PF00041; En3; 2.
SMART; SM00642; Aamy; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy; C; 1.
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hes 69; Conservative
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                                                       01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Amylopullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase type II) [Includes: Alpha-amylase (EC 3.2.1.1) (1.4-alpha-D-glucan glucanohydrolase); Pullulanase (EC 3.2.1.1) (1.4-alpha-D-glucan glucanohydrolase); Alpha-dextrin endo-1,6-alpha-glucanohydrolase))
                                                                                                                                                                                                                                                                                                                                                                                                             (Clostridium thermosulfurogenes): molecular analysis of the gene, attachment to the cell surface.";

J. Bacteriol. 176:329-3302(1994).

-! CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

-! CATALYTIC ACTIVITY: Hydrolysis of (1.-s)-alpha-blucosidic linkages in pullulan and in amylopectin and glycogen, and the alpha and beta-limit dextrins of amylopectin and glycogen.

-! SUBCELLULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS A S-LAYER ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- PTM: GLYCOSYLATED.
-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
-1- SIMILARITY: Contains 2 fibronectin type III domains.
-1- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase, Glycosidasë, Carbohydrate metabolism, Signal, Repeat,
Multifunctional enzyme, Glycoprotein.
                                                                                                                                                                                                                                                                                                                                   STRAIN=DSM 3896 / EM1;
MEDILNE=9425999; PubMed=8195085;
Matuschek M., Barchhardt G., Sahm K., Bahl H.;
"Pullulanase of Thermoanaerobacterium thermosulfurigenes EM1
                                                                                                                                                                                                                                   Bacteria, Firmicutes; Clostridia, Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBRONECTIN TYPE-III 1.
                                                                                                                                                                                              Thermoanaerobacter thermosulfurogenes (Clostridium
                                                                                                                                                                                                                                                         Thermoanaerobacteriaceae; Thermoanaerobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
AMYLOPULLULANASE.
PRT; 1861 AA
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InterPro; IPR006048; Alpha amyl_C.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR003961; FN_III.
InterPro; IPR004185; Glyco_hydro_13IG.
InterPro; IPR004183; Glyco_hydro_13N.
InterPro; IPR004193; Glyco_hydro_13N.
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Pfam; PF02806; alpha-amylase C; 1
Pfam; PF02903; alpha-amylase N;
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Pfam, PF02922; isoamylase N; 1.
Pfam, PF00395; SLH; 3.
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                                      (Rel. 30, Created)
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SMART; SMO0632; Aamy C; 1.
SMART; SM00060; FN3; 2.
STANDARD;
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                                                                                                                                                                                                                  thermosulfurogenes).
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1034 HIIGVDKPTEDIYAEVWADGLTNSTGQGPNMIAQLGYKYV-----SGTVYDSVYGSV-- 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LSFYVVP---SDDLİKPTAPYLNQPGTESSRVSLTWNPSTDNVGIYDYEIYRSDGGT 1199
                                                                                                                                                                                                                                                                   1086 YNSVYGVDDSGFTWVNAQYVGDIGNNDQYKASFTPDKIGQWEYLMRFSDNQGQDWITTST 1145
                                                                                                                                                                                                                                                                                                       101 HV------KYKIEWLNGLS------YVGDFWNRSHLIADSLGGDALR 135
                                                                                                                                                                                                                                                                                                                                                               136 VNAVIGIRIQ-----NVGGRDQ-----KGG-----MRYTEQRAQEWLEANR 171
                                                                                                                                                                                                                       OAPSNVVVTSGNGKV---DLSWLQSDGATGYNIYRSSVEGGLYEKIASNVTETTFEDANV 987
                                                                                                                                                                                            51
                                                                                                                                                                                                                                                    52 ----DILY--SKLDELGRIRTARGTLIYANVEGSYGVRQSFGKNQNPAGWTGN----PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary sequence of the alpha-toxin gene from Staphylococcus aureus
                                                                                                                                                                 Gaps
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                                                                                                                                                                 82; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                        172 DGYLYYEVAPIYNADELI-PRAVVVSM-------OSSDN----
                                                                                                                                    8.0%; Score 97; DB 1; Length 1861; 21.4%; Pred. No. 2.4;
                                                                                           34 D -> E (IN REF. 1; AAB00841).
206104 MW; 06C23070E453B574 CRC64;
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TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
           SIMILARITY.
SIMILARITY.
SIMILARITY.
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FIBRONECTIN
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SLH 1.
SLH 2.
SLH 3.
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1861 AA;
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Walker B., Bayley H.;

"Key residues for membrane binding, oligomerization, and pore forming activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin identified by cysteine activity of staphylococcal alpha-hemolysin modification.";

1 baiol. Chem. 270:23065-23071[1955].

1 baiol. Chem. 270:23065-23071[1955].

1 clandry The Release of Low-Molecular Weight Molecules AND RESULTING TO AN EVENTUAL COMMONIC LYSIS. HEPTAMER OLIGOMERIZATION AND PORE FORMATION IS REQUIRED FOR LYTIC ALGOMERIZATION CONTINUED TO ANGSTROMS IN DIAMETER.

1 cloud ANGSTROMS IN LENGTH AND UP TO 100 ANGSTROMS IN DIAMETER.

2 cloud Repeated to the Complex IS TRANSLOCATED ACROSS THE BILAYER, PROBABLY VIA THE GLY-RITH DOWAIN OF EACH STRAND.

2 cloud Repeated to the Complex of the Composed of A CAP DOMAIN AND THE AMINO LATCHES OF EACH STRAND.

2 cloud Repeated to the Complex of the Composed of A CAP DOMAIN AND THE AMINO LATCHES OF EACH STRAND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Histidine residues near the N-terminus of staphylococcal alpha-toxin as reporters of regions that are critical for oligomerization and pore formation.";
                                      X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
STRAIN=Wood 46 / ATCC 10832;
MEDINE=97102581; PubMed=8943190;
SONG L., Hobaugh M.R., Shustak C., Cheley S., Bayley H., Gouaux J.E.;
"Structure of staphylococcal alpha-hemolysin, a heptameric
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94222552; PubMed-8168947; Menaies B.E., Kernodle D.S.; "Site-directed mutagenesis of the alpha-toxin gene of Staphylococcus aureus: role of histidines in toxin activity in vitro and in a murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTOMER), 7 RIM REGIONS WHOSE PROTRUDING STRANDS MAY INTERACT WITH THE MEMBRANE BILAYER, AND THE STEM DOMAIN (52 ANGSTROMS IN LENGTH, 26 ANGSTROMS IN DIAMETER) WHICH FORMS THE TRANSMEMBRANE
                                                                                                                                                                                                                                                                      Walker B., Krishnasastry M., Zorn L., Bayley H.; "Assembly of the oligomeric membrane pore formed by Staphylococcal alpha-hemolysin examined by truncation mutagenesis."; J. Biol. Chem. 267:21782-21786(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94245329; PubMed=8188346;
Jursch R., Hildebrand A., Hobom G., Tranum-Jensen J., Ward R.,
Kehoe M., Bhakdi S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE AEROLYSIN FAMILY.
J. Biol. Chem. 267:10902-10909(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 7AHL; 14-JAN-98.
InterPro; IPR005831; Aer hem.
InterPro; IPR005830; Aer hem leuk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infect. Immun. 62:1843-1847(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infect. Immun. 62:2249-2256(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96032742; PubMed=7559447;
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                                                                                                                                                                                      Science 274:1859-1866(1996).
                                                                                                                                                                     transmembrane pore
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                                                                                                          H->R: NO OLIGOMERIZATION NOR HEMOLYTIC ACTIVITY.
                                                                                                                       H->L: 7% OF NORMAL HEMOLYTIC ACTIVITY.
H->L: 16% OF NORMAL HEMOLYTIC ACTIVITY
H->L: 46% OF NORMAL HEMOLYTIC ACTIVITY
                                                                                                  H->L: NO OLIGOMERIZATION NOR HEMOLYTIC
                                                                                       CLEAVAGE OF MONOMERS BY PROTEINASE K (MAJOR SITE).
                                                            (MINOR SITE).
CLEAVAGE OF MONOMERS BY PROTEINASE
                                                       CLEAVAGE OF MONOMERS BY PROTEINASE
                                                                            CLEAVAGE OF MONOMERS BY PROTEINASE
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Pred. No. 0.46;
                                                                                                                                                                                                                                                                                                                                                                                       35904 MW; 6711C415DF7EBF30 CRC64;
                                            ALPHA-HEMOLYSIN.
                                                                       (MAJOR SITE)
InterPro; IPR001340; Hemlyan pore.
InterPro; IPR003963; Staph blcn_txn.
Pfam; PR01117; Aerolysin; I.
PRINTS; PR01468; BICOMPNTOXIN.
TIGRRAMS; TIGR01002; hlyll; 1.
PROSITE; PS00274; AEROLYSIN; 1.
Hemolysis; Toxin; Signal; 3D-structure.
                                                                                                       ACTIVITY
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                                           319
169
160
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319 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                  218
                                                                                                            76 VEGSYGVROSFGKNONPAGWIGNPNHVKYKIEWL-NGLSYVGDFWNRSHL-----IA 126
                                                                                                                                  198 NNMVNQNWGPYDRDSW----NPVY-GNQLFMKTRNGSMKAADNFLDPNKASSLLSSGFS 251
                                                                                                                                                                                         ----- RDQKGGMR--Y 158
                                                                                                                                                                                                                           144 YGFNÖN-----VTGDDTGKIGGLIGANVSIGHTLKYVQPDFKTILESPTDKKVGWKVIF 197
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                                     ---ILYSKLDELGRTRTARGTLTYAN 75
                                                                                                                                                                                                                                                                  TEORAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMOSSDNTINEKVLVYNTANGYT
                                                             STRAIN=Enterotoxigenic; MEDLINE=89330163; Pubmed=2569152; MEDLINE=89330163; Pubmed=2569152; Med. Pel H.J., Willahaw G.A., Kusters J.G., van der Zeijst B.A.M., Gaastra W.; "The mucleotide sequence of the first two genes of the CFA/I fimbrial operon of human enterotoxigenic Escherichia coli."; Microb. Pathog. 6:297-309(1989).
 Gaps
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Jordi B.J.A.M., Willshaw G.A., van der Zeijst B.A.M., Gaastra W.;
Jordi B.J.A.M., Willshaw G.A., van der Zeijst B.A.M., Gaastra W.;
"The complete nucleotide sequence of region 1 of the CFA/I fimbrial operon of human enterotoxigenic Bscherichia coli.";
DNA Seq. 2:257-263(1992)
-1- FUNCTION: MAY SERVE AS ANCHOR FOR THE FIMBRIAE IN THE OUTER
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01-AUG-1992 (Rel. 23, Last annotation update)
CFA/I fimbrial subunit C precursor (Colonization factor antigen
: 99
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CFA/I FIMBRIAL SUBUNIT C. ; EC4C626DA9B718B7 CRC64;
88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen; Signal; Fimbria; Outer membrane; Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                869 AA
Mismatches
                                   DSPNYYKTLGTSQITPALFPKAGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%; Score 91.5;
                                                                                                                                                                                     127 DSLGGDALRVNAVTGTRTQNVGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae; Escherichia
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last seq
01-AUG-1992 (Rel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97830 MW;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                         INY 221
                                                                                                                                                                                                                                                                                                                                                                               PDF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid NTP513.
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ID CFAC_ECOLI
AC P25733;
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Streptococcus mutans."
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                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        NCBI_TaxID=1309;
                                                                         YT 218
                                                                                                YT 266
                                                                                                                                                                                                                                          GTFB OR SMU
                                                                                                                                                                                                                                                                                                                            STRAIN=GS-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogen.
      162
                                                                          217
                                                                                                  265
                                                                                                                                               GTFB_STRMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----YTEQRAQEWLE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 GOLVYGKADGSLGMLTDFTDIMAYHGNEAG----NKLAAADRTDNNLSYVGSF---- 161
                                         75 NVEGSY-----GVRQSF-----GKNQNPAGWTGNPNHVKYK-----IEWLN 110
                                                       489 TLGYSDTYSESVYKSHILSE------YGFYNQNIYKGRTQR--WQLTSSTSLKW 534
                                                                                                                                    167 LEANRDGYLYYEVAPIYNAD--ELIPR----AVVVSMQSSDNTINEKVLVYNTANGYTIN 220
                                                                                                                                                   111 GLSYVGDFWN---RSHLIADSLGGDALRVNAVTGTRTQNV-GGRDQKGGMRYTEQRAQEW 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96326353; PubMed=8759872; Welch T.J., Bartlett D.H.; Welch T.J., Bartlett D.H.; Isolation and characterization of the structural gene for OmpL, a "Isolation and characterization of the structural gene for OmpL, Photobacterium species strain 859."; J. Bacteriol. 178:5027-5031(1996)
                    65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential).
-!- INDUCTION: IN RESPONSE TO ELEVATED HYDROSTATIC PRESSURE.
                                                                                                                                                                                                                                                                                                                                                  Photobacterium profundum (Photobacterium sp. (strain SS9)).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 341;
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                   46; Indels
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Probom; PD000808; OMP 2; 1.
Transmembrane; Porin; Signal; Outer membrane.
SIGNAL
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                                                                                                                                                                                                                                                                                         (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
7.4%; Score 90; DB 1
Best Local Similarity 25.3%; Pred. No. 1.1;
Matches 46; Conservative 11; Mismatches
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        Pred. No. 2.8; ; Mismatches
                                                                                                                                                                                                                                                                     341
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InterPro; IPR003229; OMP_2.
InterPro; IPR001702; Porin_Gram-ve.
22.3%; ---
                                                                                                                                                                                                                                                                                                                             Porin-like protein L precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 AA; 36672 MW;
                    41; Conservative
                                                                                                                                                                                                                                                                     STANDARD;
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         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                     YHNG 224
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=74109;
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15-DEC-1998
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Q52581;
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                    Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                 ---DLNGDNLTVKA-----NYVFGGSDENEGYSAAAMYAMDMGLGFGAGYGEQDGQSSKN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parnogen.";

Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

-i- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT

TO PLAY A KER ROLLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
OF THEIR ABILITY TO ADHERE TO SNOCTH SURFACES AND MEDIATE THE
AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-i- CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl} (N) = D-
fructose + {(1,6)-alpha-D-glucosyl} (N+1).

-i- SUBCELLULAR LOCATION: Secreted.

-i- DISEASE: DENTAL CARIES.

-i- DISEASE: DENTAL CARIES.

-i- SUBCELLULAR GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES
WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J., Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y., Li S., Zhu H., Najar P., Lai H., White J., Roe B.A., Ferretti J.J.; "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                 169 ANRD-----GYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLV----YNTANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sobue S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO A GLUCAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kimura S., Hamada S.;
"Molecular analyses of glucosyltransferase genes among strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shiroza T., Ueda S., Kuramitsu H.K.; "Sequence analysis of the gtfB gene from Streptococcus mutans."; J. Bacteriol, 169:4263-4270(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujiwara T., Terao Y., Hoshino T., Kawabata S., Ooshima T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME BINDING PROTEIN FROM S.MUTANS. SIMILARITY: Contains 10 cell wall binding repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTFB STRMU STANDARD; PRT; 1476 AA. P08987; 069391; 069387; 069396; 069396; 01.NOV-1988 (Rel. 09, Created) 28-FED-2003 (Rel. 41, Last sequence update) 15-SED-2003 (Rel. 42, Last annotation update) Glucosyltransferase-I precursor (EC 2.4.1.5) (G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=MT4239 / Serotype C, MT4245 / Serotype
STRAIN+67 / Serotype E, and MT8148 / Serotype C;
MEDLINE-98231643; PubMed=9570124;
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STRAIN=UA159 / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
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3TFB OR SMU.1004.
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1476 AA; 165846 MW; 9C6E09F731B4CBCF CRC64;

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S (IN STRAINS GS-5, MT4245, MT4251,
7 AND MT8448).
N (IN STRAIN MT4251).
N (IN STRAIN MT4251).
D (IN STRAIN GS-5, MT4467 AND
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S -> Y (IN STRAIN WT4239).
H -> Y (IN STRAIN WT4251).
E -> K (IN STRAIN WT4251).
E -> K (IN STRAIN WT4251).
R -> P (IN STRAIN WT4239).
R -> P (IN STRAIN WT6148).
R -> H (IN STRAIN WT6148).
Y -> H (IN STRAIN GS-5, WT4239, WT4467).
Y -> H (IN STRAINS GS-5, WT4239, WT4467).
                                                                                                                                                                                                                                                                                                                                                                                           STRAINS GS-5, MT4245, MT4251, MT8181).
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AND MT8148).
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H (IN STRAINS GS-5, MT4239, MT4467
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AND MT8148).
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(IN REF. 1).
H -> L (IN REF. 1).
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                                                                 EMBL; D88654; BAA26105.1; --
EMBL; D88657; BAA26109.1; --
EMBL; D89666; BAA26113.1; --
EMBL; D89977; BAA26119.1; --
EMBL; AE014940; AAN58705.1; --
EMBL; AE014940; AAN58705.1; --
EMBL; PR0473; CW binding.
InterPro; IPR003318; Glyco, hydro, 70.
Pfam; PF01473; CW binding.1; 1.
Pfam; PF02324; Glyco hydro, 70; 1.
Transferase; Glycosyltransferase; Signal; Repeat; Dental caries;
                                                                                                                                                                                                                                                                    GLUCAN-BINDING (APPROXIMATE)
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STRAIN GS-5).
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CATALYTIC (APPROXIMATE)
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X TANDEM REPEATS.
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 tities requires a license agreement (send an email to license@isb-sib.ch)
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EMBL; D88651; BAA26101.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1296 NGYAVTGARTINGQHLYFRANGVQVKGEFVTDRHGRISYYDGNSGDQIRNRFVRNAQGQW 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1356 FYFDNNGYAVTGARTINGQHLYFRANGVQVKGEFVTDRYGRISYYDSNSGDQIRNRFVRN 1415
                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                        ---AVTGTRTQN------QRAQ-EW
                                                                                                                                                               5 VSNDVVLNDGASKYLNEALAWIFNDSPNY-----YKTLGTSQITPALFPKAGDI
                                                                                                                                                                                                                                                                                                                                                                                                                             ---NPNHVKYKIEWLNGLSYVGDF-WNRSHLIA--DSLGGDALRVN-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 LEANRDGY------LYYEVAPIYNADELIP----RAVVVSMQSSDNTINEKV--
                                                                                                                                                                                                                                                                                                54 LYSKLDELGR-----TRIARGILIYANVEGSYGVROSFGKN------QNPAGWIG-
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manchester virus (Human enteric calicivirus).
Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93390791; PubMed=7661689;
Liu B.L., Clarke I.N., Caul B.O., Lambden P.R.;
Liu B.L., Clarke I.N., Caul B.O., Lambden P.R.;
Liuman enteric calicivitues have a unique genome structure and are distinct from the Norwalk-like viruses.";
Arch. Virol. 140:1345-1356(1995).
-!- FUNCTION: P2C IS IMPORTANT IN RNA REPLICATION (BY SIMILARITY).
-!- FUNCTION: THE CYSTEINE PROTEASE IS THE PROTEASE RESPONSIBLE FOR THE POST-TRANSLATIONAL PROCESSING OF THE POLYPEPTIDE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAINS SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS. SIMILARITY: TO PICORNAVIRUS POLYPEPTIDES. SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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                                                                                                  36; Mismatches 107; Indels 105;
                                 Length 1476;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: RNA-directed RNA polymerase (EC 2.77.48); Thiol protease 3C (EC 3.4.22.-); Helicase protein); Coat protein]
                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 2208 AA.
                                 7.3%; Score 88.5; 21.3%; Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1416 AQGQWFYFDNNGYAV 1430
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Query Match
Best Local Similarity 21....
Best Local Sommit Conservative
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Q69014;
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the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                             BY SIMILARITY.
9863E58C526C85D7 CRC64;
                                                                                                                                                                  InterPro; IPR002692; Penicil amidase.
Pfam; PF01804; Penicil amidase; 1.
Hydrolase; Antibiotic resistance; Zymogen; Signal.
SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 23, Created)
(Rel. 23, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                            7.2%; Score 88; DB 1
20.6%; Pred. No. 5.1;
ive 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1047 AA.
                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                92113 MW;
                                                                                                          EMBL; L04471; AAA22077.1; -.
                                                                                                                                                                                                                                                                                                                                                            20.6%;
                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                            I39665; I39665.
                                                                                                                                                                                                                                                                              266
266
366
302 AA;
                                                                                                                                         HSSP; P06875; 1AJQ.
MEROPS; S45.001; -.
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es 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 213
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01-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 VKYKIEWLNG----LSYVGDFWNRSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 YTEORAQEWLEANRDGYLYYEV---APIYNADELIPRAVVVSMQSSDNTINEKVLVYNTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 41, Last aequence update)
Penicillin G acylase precursor (EC 3.5.1.11) (Penicillin G amidase)
(Penicillin G amidohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: Penicillin + H(2)0 = a fatty acid anion +
                                                                                                                                                                                       Polyprotein; Transferase; RNA-directed RNA polymerase; Hydrolase;
Thiol protease; Helicase; ATP-binding; Coat protein.
??? HELICASE (P2C-LIKE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Konstantinovic M., Marjanovic N., Ljubijankic G., Glisin V.; "The penicillin amidase of Arthrobacter viscosus (ATCC 15294)."; Gene 143:79-83(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     996 IGYGVHIGNGNVITVTHVAS-----TSDEVNGSAFKITRTVGETT----
                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 2208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Micrococcineae, Micrococcaceae, Arthrobacter.
                                                                                                                                                                                                                                                   RNA-DIRECTED RNA POLYMERASE.
COAT PROTEIN.
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                1097 PROTEASE (BY SIMILARITY).
1112 PROTEASE (BY SIMILARITY).
AA; 242736 MW; 3E299D5BA20E45DC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                          19.5%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                               7.3%; Score 88.5;
19.5%; Pred. No. 17
                                InterPro; IPR000665; RNA_helicase.
InterPro; IPR007065; RNA_pol_DS_PS.
InterPro; IPR007055; RNA_pol_P3D.
InterPro; IPR007094; RNA_pol_P3D.
Pfam; PF00915; Calici_coat; I.
Pfam; PF00680; RNA_dep_RNA_pol; I.
Pfam; PF00680; RNA_dep_RNA_pol; I.
Pfam; PF00910; RNA_helicase; 1.
                 Endoptase C24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 15294;
MEDLINE-94259306; PubMed-8200542;
                                                                                                                                                          PRINTS; PR00916; 2CENDOPTASE.
PRINTS; PR00918; CALICVIRUSNS.
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    Calici
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les 38; Conserv
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P31956;
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ACT SITE
SEQUENCE
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Matches
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쉱 ò g G 8 g ઠે the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ 557 617 -----ADEL----IPRAVV-----VSMQSSD----NTINEKVLVYN 212 396 ISRDETNKVAYSKYVSFRGTEAQSMSAYMKANWAKNLKEFENAASEYTMSLNWYYADKKG 455 T----QNV-----GGRDQKGGMRYTEQRAQEW----LEANRDGYLYYEVAPIYN 184 618 EWWINLHDKLFMDELGDFYGITKEITDHRYGASLAYKNISKESTNYKWVNVDQEKIIMES 677 92 506 VVNWNNKPSK----EWVNGEYSY---YWGEDNRVQQYINGMEARGKVTLEDINEINYTA -AGWTGNPNHVKYKIEWLNG-LSYVGDFWNRSHLIADSLGGDALR------VNAVTGTR 558 SFAQLRANLFKPLLIDVLDKNKSTNGNYTYLIEKLEEWNNLKEDENKDGYYDAGIAAFFD 456 DIAYYHVGRYPVRNNKIDE--RIPTP-GT-----GEYEWKGFIPFKENPHVINPKNGY 5 VSNDVVLNDGASKYLN----EALAWTFNDSPNYYKTL-----GTSQITPAL----PPKAG Gaps MEDINE=90156504; PubMed=2304139; Johnson P.T., Johnson P.K., Fomgagard A., Allan J., Gravell M., London W.T., Johnson P.K., Tensch V.M.; Simian immunodeficiency viruses from African green monkeys display unusual genetic diversity."; J. Virol. 64:1086-1092(1990).
J. Virol. 64:1086-1092 (1990). POL polyprotein [Contains: Protease (Refropepsin) (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)] PENICILLIN G ACYLASE ZYMOGEN.
PENICILLIN G ACYLASE ALPHA SUBUNIT.
SPACER PEPTIDE.
SPACER PEPTIDE.
PENICILLIN G ACYLASE BETA SUBUNIT. 88; Indels 110; DILY------SKLDELGRIRTARGTLTYANVEGSYGVROSFGKNONP-DB 1; Length 802; Simian immunodeficiency virus (AGM155 isolate) (SIV-AGM) Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11727;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 -NHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRY 158
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                       CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate + {DNA}(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                  PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
                                                                                                                                DETERMINED.
MISCELLANEOUS: THE 155 ISOLATE IS FROM A MONKEY IMPORTED FROM
                                                                                                                                                                                                                               SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO KNOWN AS THE RETROPEPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 GDILYS-KLDELGRTRTARGTLTYANVEGSYGVRQSFGKNONPAGWTGNP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00141; ASP PROTEASE; 1.
PROSITE; PS00141; ASP PROT RETROV; 1.
AIDS; POLYPTOTE411; Hydrolase; Asparty1 protease; Endonuclease;
Nuclease; Transferase; RNA-directed DNA polymerase.
ACT SITE 113 BY SIMILARITY.
SEQÜENCE 1047 AA; 118871 MW; A38DDDA39F268EE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 87.5; DB 1; Length 1047; 84.4%; Pred. No. 7.9; ve 16; Mismatches 48; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-FRB-1996 (Rel. 33, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
GDLutamate dehydrogenase (EC 1.4.1.3) (GDH).
GDHA OR GDH OR PF1602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR001995; Aspprotease rtrv.
Interpro; IPR001969; Aspprotease site.
Interpro; IPR001037; Integrase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003308; Integrase_Zn.
InterPro; IPR002156; RNaseH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00552; integrase; 1.
Pfam; PF02022; Integrase Zn; 1.
Pfam; PF00075; rnaseH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEKKVOREPPFEWM----GY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro; IPR001584; Rve.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00077; rvp; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00665; rve;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrococcus furiosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P03366; 1HRH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00078; rvt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus.
NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; A02.003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHE3 PYRFU
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DHE3_PYRFU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scandurra R., Rice D.W.; "The structure of Pyrococcus furiosus glutamate dehydrogenase reveals a key role for ion-pair networks in maintaining enzyme stability at
                                                                              archaeon Pyrococcus furiosus: sequence, transcription and analysis of the deduced amino acid sequence."; Gene 132:143-148(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structure 3:1147-1158(1995).
-!- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NAD(P)(+) = 2-
oxoglutarate + NH(3) + NAD(P)H.
-!- SUBUNIT: HOMOHOXAMER.
-!- SIBILIARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
-!- SIMILIARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
STRAIN=VG.1 / DSM 3638 / ATCC 43587 / JCM 8422;
MEDLINE=96164432; Pubmed=8591026;
Yip K.S.P., Stillman T.J., Britton K.L., Artymiuk P.J., Baker P.J., Sedelnikova S.E., Engel P.C., Pasquo A., Chiaraluce R., Consalvi V.,
                                                                                                                                                             STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
MEDLINE=94338538; PubMed=8060497;
Maras B., Valiante S., Chiaraluce R., Consalvi V., Politi L.,
de Rosa M., Bossa F., Scandurra R., Barra D.;
"The amino acid sequence of glutemmate dehydrogenase from Pyrococcus
furlosus, a hyperthermophilic archaebacterium.";
J. Protein Chem. 13:253-259(1994).
                                                                  hyperthermophilic
                              3ggen R.I.L., Geerling A.C.M., Waldkoetter K., Antranikian G.,
                                                                                                                                                                                                                                                                                                          STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Watis R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence (the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADP; 3D-structure; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAD (POTENTIAL).
AW -> WA (IN REF. :
T -> K (IN REF. 2)
STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
                                                                  ఠ
                                                                      gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; T46971; JN0894.

PDB; IGTM; 11-JAN 97.

InterPro; IPR006095; GLFV dehydrog.

InterPro; IPR006095; GLFV dehydrog.

InterPro; IPR006097; GLFV dehydrog C.

InterPro; IPR006097; GLFV dehydrog N.

Pfam; PF00208; GLFV dehydrog N.

PRINTS; PR000082; GLFV dehydrog N; 1.
                                                                 'The glutamate dehydrogenase-encoding
                    4EDLINE=94010338; PubMed=8406037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M97860; AAA83390.1; -.
EMBL; AE010260; AAL81726.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extreme temperatures
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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366
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647
644
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NP BIND
CONFLICT
                                                                                                                                                  SEQUENCE
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HELIX
HELIX
TURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 VEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVG------DFWNRSHLIA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSLGG----DALRVNAVTGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 YLN-EALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTR-TARGTLTYAN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ASYTIREA----AKVLGWDG----LKGKTIAIQGYGNAGYYLAKIMSEDYGMKVVAVS
                                                                                                                                                                                                                                                                                                                                     MEDLINE=98344137; PubMed=9679194;
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 YTNPQIMAWMDE----YETIARRK-TPAFGIITGKPL-SIGGSLGRNEATARG----
                                                                                                                           Pyrococcus horikoshii.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 5:55-76(1998).
-!- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NAD(P)(+) = 2-
oxoglutarate + NH(3) + NAD(P)H.
-!- SUBUNIT: Homohexamer (By similarity).
-!- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.1%; Score 87; DB 1; Length 420; 5.9%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72; Indels
                                                                                                                                                                                                                                                Gonzalez J.M., Robb F.T., Kato C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1198BEC2681B5AA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; FW0119; LULIN.
INTERPRO; IPR006095; GLFV dehydrog.
INTERPRO; IPR006095; GLFV dehydrog_C.
INTERPRO; IPR006097; GLFV dehydrog_N.
Pfam; PF002009; GLFV dehydrog_N.
Pfam; PF002012; GLFV dehydrog_N.
PRINTS; PR00082; GLFDHDRGNASE.
PROSITE; PS00074; GLFV DEHYDROGENASE; 1.
Oxidoreductase; NAD; NADP; Complete proteome.
ACT SITE 105 105 NAD (POTENTIAL).
NP BIND 220 226 NAD (POTENTIAL).
                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamate dehydrogenase (EC 1.4.1.3) (GDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF035935; AAB99956.1; -.
EMBL; AP000006; BAA30705.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 25.9%;
Matches 56; Conservative
STANDARD;
                                                                                                       GDHA OR GDH OR PHIS93
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                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=53953;
DHE3 PYRHO
                                                                                                                                                                                                                                     STRAIN=JA1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 VEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVG------DFWNRSHLIA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSLGG----DALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 YLN-EALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTR-TARGTLTYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- ASYTIREA----AKVLGW----DTLKGKTIAIQGYGNAGYYLAKIMSEDFGMKVVAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.1%; Score 87; DB 1; Length 420; 25.9%; Pred. No. 2.7; tive 29; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47114 MW; 673DB20F8764A93C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 YNADELIPRAV - VVSMQSSDNTINEKVLVYNTANG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.93
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416
420 AA;
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RESULT 13 DHE3_PYRHO

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                                                                                                                   Homo sapiens (Human)
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Best Local Similarity
Matches 30; Conserv
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                                             014646;
15-JUL-1998 (
15-JUL-1998 (
28-FEB-2003 (
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                                   HUMAN
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CHD1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                          EM-----YQNEASRILINQKLKDAAKKQNKPWLFSAYSPGKILLSDGRTGE--- 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELGRIRIARGILIYANVEGSYGVRQSF---GKNQNPA---------GWIGNPNH 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 VKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            919 -KFDNPVLVGRSYI---LKLAHLVEDKI--HARSTGPYSLITQQPVGGKSQNGGQRFGEM 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 SNDVVLND-GASKYLNEALAWIFNDSPNYYKTLGTSOITPALFPKAGDILYSK----LD 59
                                                                                                                                                                                                                                     Mangahas J.L., Cattolico R.A., Reynolds A.E.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                       SUBUNIT: In chloroplasts, the RNA polymerase is composed of four subunits: alpha, beta, beta', and beta".
SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymerase, Transcription, Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAGEW-LEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79; Indels
                                                                                                                                                                                          Eukaryota; stramenopiles; Raphidophyceae; Heterosigma
                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta chain (RC 2.7.7.6).
183 YNADELIPRAV--VVSMQSSDNTINEKVLVYNTANG 216
            PRT; 1116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.1%; Score 86.5; D
4.1%; Pred. No. 11;
.ve 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPRO1572; RNA pol B. Pfam; PF04563; RNA pol Rpb2 1; 1. Pfam; PF04561; RNA pol Rpb2 2; 1. Pfam; PF04561; RNA pol Rpb2 2; 1. Pfam; PF04562; RNA pol Rpb2 6; 1. Pfam; PF04560; RNA pol Rpb2 7; 1. PROSTE; PS01166; RNA POL BETA; 1. Transferase; DNA-directed RNA polym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125818 MW;
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PIR, S41915, S41915.
HSSP, Q9KWU7, 1HQM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 24.1%; 55; Conservative 1
                                                                                 STANDARD;
                                                                                                                                                                  Heterosigma carterae.
                                                                                                                                                                                                 NCBI_TaxID=28465;
                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                       SUBSTRATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0004003; F:ATP dependent DNA helicase activity; TAS.
GO; GO:0007001; P:chromosome organization and biogenesis (sen. .;
GO; GO:0006357; P:regulation of transcription from Pol II pro. .;
InterPro; IPR000953; Chromo.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
InterPro; IPR00330; SNF2_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Wooded T., Babrai M.A., Baxevanis A.D., Hieter P., Collins F.S.;
"Characterization of the CHD family of proteins.";
Proc. Natl. Acad. Sci. U.S.A. 94:11477(1997).
-!- FUNCTION: SEQUENCE-SELECTIVE DNA-BINDING PROTEIN. COULD PLAY AN IMPORTANT ROLE IN GENE REGULATION.
-!- SUBCELLIAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
-!- SIMILARITY: Contains 2 chromo domains.
                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PP00385; chromo; 2.
Pfam; PP00385; chromo; 2.
Pfam; PP00271; helicase C; 1.
Pfam; PP00171; helicase C; 1.
SMART; SM00298; CHRÖMO; 2.
SMART; SM00490; HELICC; 1.
PROSITE; PS00598; CHROMO_1; 2.
PROSITE; PS00599; CHROMO_2; 2.
DNA-binding; AIP-binding; Helicase; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 X 5 AA REPEATS OF H-S-D-H-R.
                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                           15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chromodomain-helicase-DNA-binding protein 1 (CHD-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
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DEAH BOX.
PRT; 1709 AA.
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23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.1%; Score 86.5;
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HSSP; P23197; 1AP0.
                                                              (Rel. 36, Created)
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121 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLE-ANRDGYLYYE- 178	334 TEETLKQQNVRGMKKLDNYKKKDQETKRMLKNASPEDVEYYNC 376	179VAPIYNADELIPRAVVVSMQSS 200	377 QQELTDDLHKQYQIVGRIIAHSNQKS 402
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	VAPIYNADELIPRAVVVSMOSS
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³⁷⁷ QQELTDDLHKQYQIVGRIIAHSNQKS 402

Search completed: January 5, 2004, 18:39:13 Job time : 20.3996 secs

Q8e0p2 streptococc Q8e5u4 streptococc Q8evt23 enterococc Q8dvt23 enterococc Q8nt23 enterococc Q8nt26 erreptococc Q8z161 helicobacte Q8zm0 ralstonia s Q8zm0 ralstonia s Q9zv12 ralstonia s Q9zv12 ralstonia s Q9xs12 ralstonia s Q8xs15 ralstonia s Q8xs15 ralstonia s Q8xs15 ralstonia s Q8cs enterococc Q8xs15 ralstonia s Q8cs enterococc Q8xs15 ralstonia s Q8cs enterococc Q8ycs enterococc Q8ycs enterococc Q8ycs enterococc Q8ycs enterococc Q8ycs enterococc Q8ycs enterococc Q8ycs enterococc Q8ycs enterococc Q8ycs enterococc Q8ycs enterococc Q8ycs ralstonia s Q8xs ralstonia s

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SPECIES—S. pyogenes; STRAIN=C2038; MEDLINE=21233096; PubMed=11335140; Gerlach D., Schmidt K.H., Fleischer B.; "Basic streptococcal superantigens (SPEX/SMEZ or SPEC) are responsible for the mitogenic activity of the so called mitogenic factor MF."; FEMS Immunol. Med. Microbiol. 30:209-216(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;
MEDITRE=Z213808; PubMed=1212206;
MEDITRE=Z213808; PubMed=1212206;
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-007-2001 (TrEMBLrel. 17, Created)
01-007-2001 (TrEMBLrel. 17, Last sequence update)
01-007-2002 (TrEMBLrel. 12, Last sequence update)
Streptodornase B precursor (Mitogenic factor 25K).
DNASE OR MF OR SPYN3_1745.
Streptococcus pyogenes, and
Streptococcus pyogenes (serotype M3).
Bacteria, Firmicutes; Lactobacillales; Streptococcaeee;
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Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
EMBL; AJ295272; CAC35734.1; -.
EMBL; AE014170; AAM80352.1; -.
Signal; Complete proteome.
SIGNAL
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STREPTODORNASE B.
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Q26946
Q92ES3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus.
NCBL_TaxID=1314, 198466;
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     43
     134
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271 AA.

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EMBL; D13428; BAA02693.1;
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MEDLINE=21192684; PubMed=11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
                                                                                                           RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
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                                                        Gaps
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"Cloning, characterization and overexpression of a Streptococcus
pyogenes gene encoding a new type of mitogenic factor.";
FBBS Lett. 331:187-192(1993):
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                             271;
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                            DB 16; Length
                         100.0%; Score 1220; DB 16; Length
100.0%; Pred. No. 4e-92;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                  01-NVV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mitogenic factor precursor (Mitogenic factor, 25K).
MF OR SPY2043 OR SPYM18_2104.
Streptococcus pyogenes, and
Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaeae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A novel cloning method used arbitrarily primed PCR.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
8FD8849E3CD01352 CRC64;
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STRAIN-SF370 / ATCC 700294 / Serotype M1;
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STRAIN-MGAS8232 / Serotype M18;
MEDLINE-21927593; Pubmed=11917108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94009636; PubMed=8405402;
 271 AA; 30090 MW;
                                                     229; Conservative
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus.
NCBI_TaxID=1314, 186103;
                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
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01-NOV-1996
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  SEQUENCE
                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                   43 RQTQVSNDVVLNDGASKYLNBALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYXEAA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LGRTRTARGTLTYANVEGSYGVRQSF--GKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 LGRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 162
                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                  1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                   99.7%; Score 1216; DB 16; Length 271; llarity 99.6%; Pred. No. 8.6e-92; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNCTPTQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mit on crima pyogenes (serotype M3).
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  emergence.";
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
EMBL. AE014158, AAM79702.1; -.
Complete protecome; Hypothetical protein.
SEQUENCE 264 AA; 29333 MW; 6E395486BA309399 CRC64;
                                                                                                                                                            MITOGENIC FACTOR. 8FD89DA38A124352 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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ilarity 62.1%; Pred. No. 4.2e-51;
Conservative 25; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 AA.
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-0CT-2002 (TrEMBLrel. 22, Last ann
EMBL; AB030578; BAB16025.1; -.
EMBL; AR006625; AAK34710.1; -.
EMBL; AE010113; AAL98563.1; -.
Nuclease; Signal; Complete Proteome.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
                                                                                                                                                        44 271 M3
271 AA; 30062 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                       Local Similarity
nes 228; Conserv
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47; Gaps

Indels

Length 385;

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144

204

--PNH 101

46;

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43 TYGEYKDYYTVIGESNIDQSAFPKIYKTTERVYKGQGTSEKRVTVSDVVYNPLDGYKRST 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 QNVGNNDRKGGMQYIENKVLDHIKRNPKVHVYXKATPVYQGSELLPRAVLVSALSSDGFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 NTSSTIYAESATISNNWSIEQHPNYYHVEGKAQLDIKNFPELYRTTERVYKKSGQSTKPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 QNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 TFNDSPNYYKTLGTSQITPALFPK--------AGDILYSKLDELGRTR
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                                                                                                                                                                                                                Podbielski A., Zarges I., Flosdorff A., Weber-Heynemann J., Mnolecular characterization of a major serotype M49 group A arrentococcal Danae and (44an) ".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78; Indels
                                                                                       Podbeilski A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from Streptococcus pyogenes.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF410852; AAL02116.1; -
SEQUENCE 327 AA; 36834 MW; 62DDD3443017071F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                     Btreptococcal DNase gene (sdan).";
Infect. Immun. 64:5349-5356(1996).
EMBL; X84793; CAA59264.1; -.
SEQUENCE 385 AA; 43476 MW; 14922BOAFC3BD6D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 TARGTLTYANVEGSYGVROSFGKNONPAGW-----TGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              Query Match 32.1%; Score 391.5; DB 2; Best Local Similarity 35.0%; Pred. No. 5.5e-24; Matches 91; Conservative 38; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 NDGASKYLNEALA---WIFNDSPNYYKTLGTSQI-----
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35.0%; Pred. No. 1.7e-22;
iive 34; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 AA
                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Selotype M49;
MEDLINE-97101060; PubMed=8945587;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 NEKVLVYNTANGYTINYHNG 224
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Matches 85; Conservative
                                             SEQUENCE FROM N.A.
STRAIN=serotype M49;
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      NCBI_TaxID=1314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 WNKSHLIADSLGGDALRVNAITGTRTQNVGGRSGNGGMRYTEIKSQKWLEAHRDGYLYYE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WNIVQHPNYYIVEGKSHLNKEKFPQIYHTTEKVYRKSGQSTKRVTVSDIQYSILDGYGRS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 HVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 ORAGEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMOSSDNTINEKVLVYNTANGYTIN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 RTARGTLTYANVEGSYGVRQSFGKNONPAGWTG-------NP-----NP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21927593; PubMed=11917108; MEDLINE-21927593; PubMed=11917108; Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Vessy L.G., Musser J.M.; Genome sequence and comparative microrarray analysis of serciype MIS group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                         179 VAPIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGT 225
                                                               213 AMPIYQGNELVPRAVVVSVLSSDNTINEKVIVYNVANGYTIDYNQGT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 401; DB 16; Lengua J. Pred, No. 7.5e-25;
                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes (serotype M18).
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteome.
332 AA; 37652 MW; 58DC9F930865FBC0 CRC64;
                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Last annotation update)
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EMBL; AE010084; AAL98274.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Mismatches
                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.9%;
                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22,
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05,
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                                                                                                                                                                                          PRELIMINARY;
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01-JAN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=186103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 YHNG 224
                                                                                                                                                                                                                                                                                              Streptodornase.
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TRIARGILIYANVEGSYGVROSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSH 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 LIADSLGGDALR-VNAVTGTRTQNVGGRDQKGGMRYTEQRAQE-----WLEANRDGYLYY 177
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EMBL, AF400065; AAK92009.1; --
SEQUENCE 278 AA; 30597 MW; DBA1337649DEBBAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 QGDNEIIVNNNQPTFTTADLATT--NGP--WQT-----FSNLDQLNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%; Score 181.5; DB 2; Length 278; larity 27.1%; Pred. No. 5.8e-07; Conservative 33; Mismatches 77; Indels 57
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Hasegawa T., Torii K., Hashikawa S., Iinuma Y., Ohta M.;
Cloning and characterization of two new novel DNases from
Streptococcus pyogenes.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF461500; AAL66371.1;
SEQUENCE 252 AA; 28347 MW; 92CABBC832F5CFB8 CRC64;
                                                                                                                                                                                 Lactobacillus sakei.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI_TaxID=1599;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical membrane protein LaaO.
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Last sequence update)
Last annotation update)
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28.0%; Pred. No. 7.4e-07;
tive 37; Mismatches 80
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
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nes 63; Conservative
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Best Local Si
Matches 63;
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GAYGVVTKDMIDMSKGYREKWETNPEPSGWFRFYNRADNEEISEKEYDSRRTKSYKVTNN 162
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                                                                      VKYKI EWLNGLSYVGDFWNRSHL I ADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTBQ
                                                                                                               RAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINY
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Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mamarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
Embl. Acad. Sci. U.S.A. 99:10078-10083(2002)
Complete proteome
SEQUENCE 326 AA; 36645 MW; C9635F8A0CA6A51F CR
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29.8%; Score 363; DB 16;
Best Local Similarity 34.6%; Pred. No. 9.5e-22;
Matches 84; Conservative 34; Mismatches 79;
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01-0CT-2002 (TrEMBLrel. 22, Last seque
01-0CT-2002 (TrEMBLrel. 22, Last annot
Streptodornase (Sdn)-phage associated.
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NCBL_TaxID=198466;
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148 G---GRDQKG--GMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAV----- 193

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RESULT 8
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SEQUENCE 252 AA;
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147 GAYSGANDSNPEGMLYYENRLDSWLALHPDFWLDYKVTPIYSGNEVVPRQIELQYVGIDS 206
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STRAIN=NEMA16 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusnick C., Buchrieser C., Chevalier F., Frangeul L.,
Maadek I., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 YLYYEVAPIYNADELIPRAVVVSMQS-SDNTINEKVLVYNTANGYTINYHNGT 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                ----VVSMQSSDNTINEK----VLVYNTANGYTINYHNGTPTOK
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Purative DNase (Similar to mitogenic factor), phage
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002)
EBBL; AL766845; CAD46056.1; -.
EMBL; AL766846; CAD46556.1; -.
EMBL; AL766848; CAD46656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
GBS0382 OR GBS0712 OR GBS0997.
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NCBI_TaxID=1314, 186103;
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Q8CM17
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                           MEDILINE=21192664; PubMed=11296296; Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Sivorov A.N., Kenton S., Lai H.S., Lin S.P., Ojan Y., Jia H.G., Najar P.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 YYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGSYGVRQSFGK-NON
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S. Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Bares S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Baly J.A., Veasy L.G., Musser J.M.; Genome sequence and comparative microarray analysis of serotype MIS group A Streptococcus strains associated with acute rheumatic fever outbreaks.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chaussee M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S. Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., "Kapur V., Daly J.A., Veasy L.G., Musser J.M., "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks."

Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.1%; Score 171.5; DB 16; Length 252; 27.6%; Pred. No. 3.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 -----VVSMQSSDNTINEK----VLVYNTANGYTINYHNGTPTQK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptōcoccus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 SGELLTIRLNSNKESIDENGVTTVILENSAPNINLDYLNGTATPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 AA; 28373 MW; 71EA2332E358440D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acad. Sci. U.S.A. 99:4668-4673(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37; Mismatches
STRAIN=SF370 / ATCC 700294 / Serotype M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE0106523; AAK33665.1; -. EMBL; AE010008; AAL97446.1; -.
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99 TY-------NPVGW----H-NYNFYYKKSDGSIGKMMLMARGHLVGYQF 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 SGLNNEARNLVPETAWFNGGNFTGTNDGNT-----ASMLYYENRLDSWLANHPNYYLDY 189
                                                                                                                                        Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis sp., lactis III.403.",
Genome Res. 11.731-753 (2001).

EMBL; AE006253; AAK04254.1;
Hypothetical protein; Complete proteome.

SEQUENCE 263 AA; 28854 MW; EAA95B6FA317207C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        ------RTARGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                39 TDNSSQVSTKSLASSVKQAPLTFKNQRQMVMANTDALGRAVDSHIQLKDSQEPKVKREPL
               Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCSI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 DSLGGDALRV-----NAVIGTRTONVGGRDQKGGMRYTEORAQEWLEANRDGYLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 EVAPIYNADELIPRAV---VVSMQSSDNTINEK------VLVXNTANGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=NEM116 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                         DB 16; Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 343;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.3%; Score 150; DB 16; Length 3 clarity 25.5%; Pred. No. 0.0003; Conservative 33; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                          26 TFNDSPNYYKTLGTS-QITPALFPKAGDILYSKLDELGRT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sagalist; gbs0153; -.
Hypothetical protein; Complete proteome.
SEQUENCE 343 AA; 38877 MW; 11BF35A12D959DF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                 ch 12.6%; Score 153.5; DB 16; 1 Similarity 24.4%; Pred. No. 0.00011; 60; Conservative 26; Mismatches 85;
                                                                                                          STRAIN=1L1403;
MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766844; CAD45798.1;
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Best Local Similarity
Matches 62; Conservat
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Matches 60; Conserv
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                                                                       [1] -
SEQUENCE FROM N.A.
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                                                                                                         12;
                                                                                                                                                                                                      QNPAGWTGNPNHVKYKIEWLNGLSYVGDFW--NRSHLIADSLGG--DALRVNAVTGTRTQ 145
                                                                                                                                                                                                                                 37 LGTSQI-TPALFPKAG--DILYSKLDELGRTRTARGTLTYANV----EGSYGVRQSFGKN 89
                                                                                                                                                        QNPAGWIGNPNHVKYKIEWLNGLSYVGDFW--NRSHLIADSLGG--DALRVNAVIGTRIQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 LGTSQI-TPALFPKAG--DILYSKLDELGRTRTARGTLTYANV----BGSYGVRQSFGKN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 LGTKATETPGILPFTGSYQLVLGDLDNLQRP-----TFAHIQLKDQDEPNIKRK-GLK 98
                                                                                                                                                                                                                                                                               146 NVGGRDQKG-GMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSD 201
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STALIN-SR370 / ATCC 700294 / Serotype M1;
MEDLINE=21192684; PubMed=11296296;
Ferretti J.J., McShan W. Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Vian X., Clifton S.W., Roe B.A., McIaughlin R., Song L., White J., "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 NVGGRDOKG-GMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSD 201
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                                                                                                   65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
13.0%; Score 158.5; DB 16; Length
Best Local Similarity 31.1%; Pred. No. 4.3e-05;
Matches 55; Conservative 26; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Complete proteome.
SEQUENCE 266 AA; 30153 MW; 45475BC64C408F9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 AA; 30398 MW; 24EA4762A5DDAA5E CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
                                                       13.0%; Score 158.5; DB 1/
31.1%; Pred. No. 4.2e-05;
Live 26; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                        268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                              Q99226,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9CU50, CLEMBLE 17, C
01-UUN-2001 (TrEMBLE 1. 17, C
01-UUN-2001 (TrEMBLE 1. 17, L,
01-MAR-2002 (TrEMBLE 1. 20, L,
Hypothetical protein ybfB.
YBFB OR LLO156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative deoxyribonuclease
                                                                                             55; Conservative
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                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1314;
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                                                       Query Match
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Q9CJ50

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Search completed: January 5, 2004, 18:41:36 Job time : 55.1381 secs This Page Blank (uspto)

Perfect score:

Sequence:

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Run on:

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Sequence 6630, Ap
Sequence 4, Appli
Sequence 31088, A
Sequence 31522, A
Sequence 24124, A
Sequence 23157, A
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Sequence 24424, A
Sequence 21157, A
Sequence 14678, A
Sequence 29801, A
Sequence 30825, A
Sequence 31088, A
Sequence 15081, A
Sequence 15081, A
Sequence 20000, A
Sequence 20000, A
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Sequence 15, Appl
Sequence 15, Appl
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Sequence 7674, Ap
Sequence 1687, Ap
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Sequence 98, Appl
Sequence 79111, A
Sequence 110035,
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Sequence 6, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
NUMBER OF SEQUENCES: 16
NUMBER OF SEQUENCES: 16
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
                                                                                                                                                1. US-09-113-900-15

1. US-09-113-900-15

1. US-09-113-900-15

1. US-09-1483-032-15

1. US-09-486-203-7674

1. US-09-486-203-7674

1. US-09-484-722-1687

1. US-09-55-633-4

1. US-09-65-633-4

1. US-09-65-633-4

1. US-09-66-4761-37952

1. US-09-66-4761-37952

1. US-09-864-761-37952

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1. US-09-30-3138-15081

1. US-10-203-138-30000

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1. US-09-791-537-147417

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.25
CURRENT APPLICATION NAMBER: US/08/482,785
US-09-119-900-1
US-10-453-032-1
US-08-188-718-2
US-08-482-785-8
US-09-119-900-8
US-09-110-455-032-8
US-08-482-785-128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/08482785; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397
397
397
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3397
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576
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                                                                                                                                                    January 5, 2004, 18:38:21; Search time 51.3149 Seconds (without alignments) 762.478 Million cell updates/sec
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1 MNLLGSRRVFSKKCRLVKFS......LVSATMAVTTVTLENTALAR
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1: \cgn2 6/ptodata/2/paa/USG6 COMB.pep:*

2: \cgn2 6/ptodata/2/paa/USG6 COMB.pep:*

4: \cgn2 6/ptodata/2/paa/USG6 COMB.pep:*

4: \cgn2 6/ptodata/2/paa/USG8 COMB.pep:*

6: \cgn2 6/ptodata/2/paa/USG8 COMB.pep:*

7: \cgn2 6/ptodata/2/paa/USG82 COMB.pep:*

7: \cgn2 6/ptodata/2/paa/USG82 COMB.pep:*

9: \cgn2 6/ptodata/2/paa/USG82 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG85 COMB.pep:*

11: \cgn2 6/ptodata/2/paa/USG85 COMB.pep:*

13: \cgn2 6/ptodata/2/paa/USG85 COMB.pep:*

14: \cgn2 6/ptodata/2/paa/USG85 COMB.pep:*

15: \cgn2 6/ptodata/2/paa/USG85 COMB.pep:*

16: \cgn2 6/ptodata/2/paa/USG85 COMB.pep:*

17: \cgn2 6/ptodata/2/paa/USG85 COMB.pep:*

16: \cgn2 6/ptodata/2/paa/USG85 COMB.pep:*

17: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

16: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

17: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

18: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

19: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG95 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG99 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG99 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG99 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG99 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG99 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG99 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG99 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG99 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG99 COMB.pep:*

10: \cgn2 6/ptodata/2/paa/USG99 COMB.pep:*
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6/ptodata/2/paa/US089_COMB.pep:
6/ptodata/2/paa/US091_COMB.pep:
6/ptodata/2/paa/US091_COMB.pep:
6/ptodata/2/paa/US093_COMB.pep:
6/ptodata/2/paa/US094_COMB.pep:
6/ptodata/2/paa/US095_COMB.pep:
6/ptodata/2/paa/US095_COMB.pep:
6/ptodata/2/paa/US095_COMB.pep:
6/ptodata/2/paa/US099_COMB.pep:
6/ptodata/2/paa/US099_COMB.pep:
6/ptodata/2/paa/US099_COMB.pep:
6/ptodata/2/paa/US099_COMB.pep:
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6/ptodata/2/paa/US099_COMB.pep:
6/ptodata/2/paa/US009_COMB.pep:
6/ptodata/2/paa/US001_COMB.pep:
6/ptodata/2/paa/US101_COMB.pep:
6/ptodata/2/paa/US101_COMB.pep:
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6/ptodata/2/paa/US101_COMB.pep:
6/ptodata/2/paa/US101_COMB.pep:
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                5728757 segs, 909918778 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 8 US-08-482-785-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 203; DB 30; Best Local Similarity 100.0%; Pred. No. 4.5e-22; Matches 43; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                Query Match 100.0%; Score 203; DB 15; Best Local Similarity 100.0%; Pred. No. 4.5e-22; Matches 43; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,032
FILING DATE: 03-JUNE-2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: 23-JUNE-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pyogenes
                                                                                                                                                    ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10453032
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 95.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (818) 795-6321
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-terminal
                                                                                HYPOTHETICAL: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
43 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    california
: USA
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                                             linear
                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: PHYPOTHETICAL: NO FRAGMENT TYPE: NO ORIGINAL SOURCE:
                                         TOPOLOGY: 1i:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09119900
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Pasadena synth: California country: USA ZIP: 91001
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible CORPUTER: BATCHING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shaldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: US/08/082,845
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pyogenes US-08-482-785-1
                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32 612
REFERENCE/DOCKET NUMBER: 9521
TELEPHONE: (818) 795-4000
TELEPAX: (818) 795-631
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REPERENCE/DOCKET NUMBER: 95,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
    07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (818) 795-6321
FPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.(
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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Query Match
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 43; Conservative 0; Mismatches 0; Indels (
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GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Matina
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Peadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
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                                                                                                                                                     SOFTWARE PATENTIN FELGASE #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889 FILING DATE: 24-FEB-1995 APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGETT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 271 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
LENGTH: 271 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-482-785-8
       California
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                                                                                                                                     APPLICANT: Hara, Ayako

APPLICANT: Hara, Ayako

APPLICANT: Takeda, Yoshifumi

APPLICANT: Takeda, Yoshifumi

APPLICANT: Takeda, Yoshifumi

TITLE OF INVENTION: Mitogenic Factor, Gene Thereof and

TITLE OF INVENTION: Method of Microdetection Therefor

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart ---

STREET: 8110 Gart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 203; DB 5; Length 271; 100.0%; Pred. No. 3.6e-21; tive 0; Mismatches 0; Indels
1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22042
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPSY MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,721A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falla Church. STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08482785; GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Belei, Martina; TITLE OF INVENTION: Recombinant DNase B Deriva; TITLE OF INVENTION: Streptococcus pyogenes; NUMBER OF SEQUENCES: 16; CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION UNDRER: 28,977
REFERENCE/DOCKET NUMBER: 1422-178P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
                                                                                                              Sequence 2, Application US/08188721A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 248345
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acide
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-721A-2
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Best Local Similarity
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                                                                                      US-08-188-721A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-482-785-8
                                                                   RESULT 4
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785 FILING DATE: 07-UNN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FBB-1995
APPLICATION NUMBER: US/08/082,845
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,9612
REFERENCE/DOCKET NUMBER: 95.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-482-785-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-119-900-15
                    RESULT 8
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                                                                                                                                                                                                                                    Score 203; DB 15; Length 271; Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                 1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                                                                                                                                                              1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Pend, Patty P.-Y.
APPLICANT: Belei, warina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: 1
ADDRESSEE: Shaldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,032
FILING DATE: 03-JUNE-2003
                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: 23-JUNE-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10453032 GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: 952:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 795-4000
TELEPAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (818) 796-4000
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INFORMATION FOR SEQ 1D NO: 8EQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 43; Conservative
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                                                                                                                                                                        MOLECULE TYPE: protein US-09-119-900-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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US-10-453-032-8
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Gaps
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DB 8; Length 272;
                                           Indels
                                                                                                                                  NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAQ 45
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APPLICANT: Pang, Patty P.-Y.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCES: 18
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                           1; Mismatches
                                                                                                                                                                                                                                            Sequence 15, Application US/09119900 GENERAL INFORMATION:
    95.6%;
  Query Match
Best Local Similarity 97.6
Matches 41; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
TOPOLOGY: linear
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US-09-489-039A-7674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 91001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,032
FILING DATE: 03-UNNE-2003
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/10453032
; Sequence 15, Application US/10453032
; APPLICANT: Adams, Craig W.
; APPLICANT: Belei, Marina
; TITLE OF INVENTION: Recombinant DNase B Deriv.
; TITLE OF INVENTION: Streptococcus pyogenes
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.6%; Score 194; DB 15
97.6%; Pred. No. 8e-20;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DAIL:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: 23-JUNE-1993
ATTORNEY-AGENT INFORMATION:
NAME: FASTDER, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                              PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Faiber, Michael B.
RESISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acide
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INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.6°
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-119-900-15
                                                                                                                                                                FILING DATE:
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APPLICANT: Kovalic, David K.
APPLICANT: Show, Thomas J.
APPLICANT: Show, Yihua
APPLICANT: Show, Yihua
APPLICANT: Show, Yihua
APPLICANT: Show, Yihua
APPLICANT: Www. Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Pand
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 121351
LENGTH: 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7674, Application US/09489039A

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
SEQ ID NO 7674
LIENGTH: 308
                                                                                                                                   Gaps
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0
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                                                                                DB 30; Length 272;
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                                                                                                                                                                                      2 NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                              4 NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_24385C.1.pep
US-10-437-963-121351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 NLINFQNTFTMKFSL--FSVIALASAAMAAPAVQVQAKA 46
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41.0%; Pred. No. 8.5;
tive 6; Mismatches 15
                                                                             Query Match
95.6%; Score 194; DB 30
Best Local Similarity 97.6%; Pred. No. 8e-20;
Matches 41; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(219)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                               Sequence 121351, Application US/10437963 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 41.0%
; MOLECULE TYPE: protein US-10-453-032-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-489-039A-7674
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                    PRT
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Sequence 1687, Application US/60161932
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
CURRENT APPLICATION NUMBER: US/60/161,932
CURRENT APPLICATION NUMBER: US/60/161,932
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 2626
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1687
LENGTH: 507
                                                                                                                                                                                                                                                    Sequence 7674, Application US/10446203
SERERAL INFORMATION:
APPLICANT: Gary Breton et. al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: DEBUNDANIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/446,203
CURRENT FILING DATE: 2000-01-27
PRIOR PLILING DATE: 2000-01-27
PRIOR PLILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7674
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                                                                          Gaps
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                                                                                                                                              41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 507;
                           Score 58; DB 18; Length 308;
Pred. No. 18;
5; Mismatches 15; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GSRRVFSKKCRLVKF------SMVALVSATMAVTTVTLENTAL
                                                                                                                   ------SMVALVSATMAVTTVTLENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 NLLSAQFKSEANFSKSCLLL--TLTALVALSLAATTTTTT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NLLG----SRRVFSKKCRLVKFSMVALVSATMAVTTVTLENT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 32;
31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58; DB 30;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.6%; Score 58; Best Local Similarity 40.5%; Pred. No. Matches 17; Conservative 6; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-446-203-7674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.6%;
Best Local Similarity 34.7%;
Matches 17; Conservative
                               Query Match 28.6%;
Best Local Similarity 34.7%;
Matches 17; Conservative
                                                                                                                        5 GSRRVFSKKCRLVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Drosophila
US-60-161-932-1687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-60-161-932-1687
                                                                                                                                                                                                                                  RESULT 13
US-10-446-203-7674
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US-09-758-472-6630
; Sequence 6630, Application US/09758472
; GRNERAL INFORMATION:
; APPLICANT: Rosen et al.

RESULT 15

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COCATION: (2018)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (2018)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-758-472-6630
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28.1%; Score 57; DB 22; Length 216;
Best Local Similarity 34.3%; Pred. No. 17;
Matches 12; Conservative 13; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| ::|:|::| || :||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||:| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||::| ||
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FILE REFERENCE: PH001
CURRENT APPLICATION WUMBER: US/09/758,472
CURRENT APPLICATION WUMBER: US/09/758,472
CURRENT FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9632
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 6630
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Sequence 8, Appli
Sequence 3009, Appl
Sequence 62081, Appl
Sequence 6324, Appl
Sequence 5446, Appl
Sequence 50770, Appl
Sequence 195, Appl
Sequence 195, Appl
Sequence 106, Appl
Sequence 106, Appl
Sequence 16489, Appl
Sequence 15489, Appl
Sequence 15489, Appl
Sequence 15489, Appl
Sequence 1636, Appl
Sequence 16489, Appl
Sequence 16489, Appl
Sequence 16478, Appl
Sequence 16489, Appl
Sequence 16478, Appl
Sequence 2781, Appl
Sequence 2781, Appl
Sequence 2687, Appl
Sequence 2687, Appl
Sequence 2687, Appl
Sequence 2687, Appl
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Sequence 8, Appli
                                                                                5, 2004, 18:39:19; Search time 6.81031 Seconds (without alignments) 408.499 Million cell updates/sec
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                                                                                                                                                       203
1 MNLLGSRRVFSKKCRLVKFS......LVSATMAVTTVTLENTALAR
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                                                                                                                                                                                                                                                                                                                                                                                                 Pending Patente AA New:*

(cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/USO)
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-08-472-630-8

US-08-472-630-8

US-09-614-150A-3009

US-10-425-114A-62081

US-10-679-063-5446

US-10-679-063-5446

US-10-679-063-5344

US-10-679-063-586

US-10-679-063-1812

US-10-679-063-1812

US-10-425-114A-50060

US-10-425-114A-50060

US-10-425-114A-44778

US-09-614-150A-15478

US-09-614-150A-1818

US-10-679-063-18636

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US-09-614-150A-15249
US-10-679-063-10401
US-10-679-063-2119
US-10-679-063-6285
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                                                                                                                                                                                                                                           320769 Begs, 64697744 residues
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Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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3394
4426
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27	46	22.7	3432	9	US-10-679-063-14204	Sequence	14204, A
28	45.5	22.4	164	ø	US-10-322-696A-132	Sequence	132, App
29	45.5	22.4	164	۲	US-60-487-610-1573	Sequence	1573,
30	45.5	22.4	164	7	US-60-485-450-1001	Sequence	1001, Ap
31	45.5	22.4	227	ø	US-10-425-114A-61944	Sequence	61944, A
32	45.5	22.4	253	-	PCT-US03-32827-58	Sequence	58, Appl
33	45.5	22.4	253	9	US-10-655-873-8	Sequence	
34	45.5	22.4	253	9	US-10-322-696A-186	Sequence	186, App
35	45.5	22.4	253	9	US-10-688-845-58	Sequence	
36	45.5	22.4	253	7	US-60-487-610-1572	Sequence	1572, Ap
37	45.5	22.4	253	7	US-60-485-450-1000	Sequence	1000, Ap
38	45.5	22.4	288	S	US-09-897-516A-6710	Sequence	6710, Ap
39	45.5	22.4	488	9	US-10-679-063-12973	Sequence	12973, A
40	45	22.2	399	9	US-10-679-063-20248	Sequence	20248, A
41	45	22.2	413	9	US-10-296-115-1094	Sequence	1094, Ap
42	45	22.2	424	9	US-10-389-647-446	Sequence	
43	45	22.2	520	v	US-10-679-063-5781	Sequence	5781, Ap
44	45	22.2	533	Ŋ	US-09-614-150A-18036	Sequence	18036,
45	45	22.2	665	₂	US-09-614-150A-30417	Sequence	30417, A

ALIGNMENTS

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GENERAL INCORMATION:

GENERAL INCORMATION:

Pang, PETLY P. Y.

Belli, Marina

TITLE OF INVENTION: Recombinant DNase B Derived from Streptococcus pyogenes

NUMBER OF SEQUENCES: 16

CORRESPONDENCES: 16

CORRESPONDENCES: 16

CORRESPONDENCES: 16

CORRESPONDENCES: 16

CORRESPONDENCES: 16

CORRESPONDENCES: 16

CORPUTE: 225 South Lake Avenue, Ninth Floor

CITY: Pasaldon & Mak

STREET: 225 South Lake Avenue, Ninth Floor

CITY: Pasaldon & Mak

STREET: 225 South Lake Avenue, Ninth Floor

CITY: Pasaldon & Mak

STREET: 225 South Lake Avenue, Ninth Floor

CITY: Pasaldon & Mak

STREET: 225 South Lake Avenue, Ninth Floor

CITY: Pasaldon & Mak

STREET: 225 South Lake Avenue, Ninth Floor

CITY: Pasaldon & Mak

STREET: 235 South Lake Avenue, Ninth Floor

CITY: Pasaldon & Mak

STREET: 235 South Lake Avenue, Ninth Floor

CONDUTER: Isla PC Compatible

COMPUTER: Isla PC Compatible

COMPUTER: Isla PC Compatible

COMPUTER: Isla PC Compatible

COMPUTER: Isla PC Compatible

COMPUTER: Isla PC Compatible

COMPUTER: Isla PC Compatible

PELING DATE: (Unknown)

PILING DATE: (Unknown)

PILING DATE: (Unknown)

PILING DATE: (Unknown)

PILING DATE: (Unknown)

ATTORRY AREPITATION NUMBER: 32, 612

REGISTRATION NUMBER: 32, 612

REGISTRATION NUMBER: 32, 612

REGISTRATION NUMBER: 32, 612

REGISTRATION NUMBER: 32, 612

REGISTRATION NUMBER: 32, 612

REGISTRATION: NUMBER: 32, 612

REGISTRATION: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 amino acid

TYPOLOGY: linear

MOLECULE TYPE: MATERIATION:

NOLECULE TYPE: Period

TYPOLOGY: linear

MOLECULE TYPE: NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 amino acid

TYPOLOGY: linear

MOLECULE TYPE: Period

TYPOLOGY: linear

MOLECULE TYPE: Period

TYPOLOGY: Linear

MOLECULE TYPE: Period

TYPOLOGY: Linear

MOLECULE TYPE: SEQUENCE:

COMPUTER: SEQUENCE: CORPUTER: SEQUENCE:

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APPLICATION NUMBER: 60/191,637
FILING DATE: 2000-03-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 15
                                                              CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-03-;
NUMBER OF SEQ ID NOS: 43008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.6'
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -09-614-150A-3009
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        Length 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Recombinant DNase B Derived from
                                               0; Indels
                                                                                                                                                                                                                                                                            APPLICANT: Adams, Craig W.
Pang, Patty P.-Y.
Balei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
                                                                                        1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
                                                                                                                                 1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR
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                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 203; DB 4;
Pred. No. 1.5e-21;
      100.0%; Score 203; DB 4;
100.0%; Pred. No. 2.2e-22;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vex
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Uun-1995
CLASSIFICATION: «UNknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 203; I Best Local Similarity 100.0%; Pred. No. 1.5 Matches 43; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 95;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08472630 GENERAL INFORMATION:
                                                                                                                                                                                                                                   Sequence 8, Application US/08472630 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Adams, Craig W.
Pang, Patty P.-Y.
Belei, Marina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Pasadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
Query Match
Best Local Similarity 100.
Marches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (818)
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US-08-472-630-15
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT FILING DATE: 1090-10-7-11
PRIOR PELICATION NUMBER: 60/160,191
PRIOR PELICATION NUMBER: 60/160,191
PRIOR PELICATION NUMBER: 60/161,932
PRIOR PELICATION NUMBER: 60/161,932
PRIOR PELICATION NUMBER: 60/161,932
PRIOR PELICATION NUMBER: 60/161,932
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PRIOR PELICATION NUMBER: 60/161,932
PRIOR PELICATION NUMBER: 60/161,932
PRIOR PELICATION NUMBER: 60/161,932
PRIOR PELICATION NUMBER: 60/175,693
PRIOR PELICATION NUMBER: 60/175,693
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PRIOR PELICATION NUMBER: 60/175,693
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                                                                                                                      ZIP: 91001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.6%; Score 194; DB 4;
97.6%; Pred. No. 2.9e-20;
tive 1; Mismatches 0
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3009, Application US/09614150A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 272 amino acids
TYPE: amino acid
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APPLICANT: Zhou, Yillous
APPLICANT: Zhou, Yillous
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Natural On Sea Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICANTION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                           US-10-679-063-5446

; Sequence 5446, Application US/10679063
; GENERAL INFORMATION: Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15/52054)B
; CURRENT APPLICATION NUMBER: US/10/679,063
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/415,758
; NUMBER OF SEQ ID NOS: 27373
; ROUBER OF SEQ ID NOS: 27373
; LENGTH: 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQUENCE 6586, Application US/10679063

GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054) B
CURRENT APPLICATION UNMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2022-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NOS: 27373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52, DB 6; Length 384;
Pred. No. 10;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.6%; Score 52; DB 6; Length 384; 48.1%; Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
     169 LFKKKVSLRKVSTLVVVSFGVAVATVT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 VFSKKCRLVKFSMVALVSATMAVTTVT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 VFSKKCRLVKFSMVALVSATMAVTTVT 35
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APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.6%;
Best Local Similarity 48.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 48.1
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Zea mays
US-10-679-063-6586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Zea r
US-10-679-063-5446
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 62081, Application US/10425114A

GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: APPLICANT: Aboven E
APPLICANT: Screen, Screen, Screen, Steven E
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Screen, Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: APPLICANT: Cao, Yongwei
APPLICANT: APPLICANT: Bank I APPLICANT: Cao, TONGWEI
APPLICANT: Cao, ANDERS 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
BEQ ID NO 62081
LENGTH: 304
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US-10-679-063-6324

i Sequence 6324, Application US/10679063

i GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-15 (52024)

CURRENT APPLICATION NUMBER: US/10/679,063

PRIOR FILING DATE: 2003-10-02

PRIOR FILING DATE: 2002-10-02

NUMBER OF SEQ ID NOS: 27373

SEQ ID NO 6324
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                                                                                                                                                                             26.1%; Score 53; DB 5; Length 1471; 30.2%; Pred. No. 31; tive 10; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.6%; Score 52; DB 6; Length 304; Best Local Similarity 48.1%; Pred. No. 8.2; Matches 13; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.6%; Score 52; DB 6; Length 336;
48.1%; Pred. No. 9.1;
tive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                             1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: LIB3637-227-D4_FLI.pep
US-10-425-114A-62081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 VFSKKCRLVKFSMVALVSATMAVTTVT 35
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                                                                                                                                                                          Query Match
Best Local Similarity 30.2%
Matches 13; Conservative
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Best Local Similarity 48.1;
Matches 13; Conservative
                                                                         TYPE: PRT
ORGANISM: DROSOPHILA
US-09-614-150A-3009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea maye
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ORGANISM: Zea mays
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Length 730;

Score 51; DB 5; Pred. No. 29; 2; Mismatches

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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 195
LENGTH: 730
                                                                                                                                                                                                                                                                                                                                                                                                                                2 NLLGSRRVFSKKCRLVKFS 20
                                                                                                                                                                                                                                                                                                                      25.1%;
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                                                                                       TYPE: PRT ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                            US-09-614-150A-195
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Sequence 195, Application US/09614150A

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOON 28

CURRENT APPLICATION NUMBER: US/09/614,150A

CURRENT FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-11-28

PRIOR FILING DATE: 1999-11-28

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TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 312
LENGTH: 398
                                                                                                                                                                                                                           25.6%; Score 52; DB 6; Length 394;
48.1%; Pred. No. 11;
ive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.6%; Score 52; DB 6; Length 398; Best Local Similarity 48.1%; Pred. No. 11; Matches 13; Conservative 4; Mismatches 10; Indels
                                                                                                                                      ; OTHER INFORMATION: Clone ID: 700221931_FLI.pep
US-10-425-114A-50770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure

LOCATION: (1).(398)

// OTHER INFORMATION: unsure at all Xaa locations

US-10-679-063-3812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-679-063-3812; Sequence 3812, Application US/10679063; GENERAL INFORMATION:
                                                                                                                                                                                                                                                Local Similarity 48.1
hes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Oryza sativa
                                                 TYPE: PRT
ORGANISM: Zea mays
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; SEQ ID NO 50770
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Best Local S:
Matches 13
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APPLICANT: LUBBERS, MARK WILLIAM
APPLICANT: LUBBERS, MARK WILLIAM
APPLICANT: LUBBERS, MARK
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES,
TITLE OF INVENTION: MATERIALS INCORPORATING THEM, AND METHODS FOR USING
TITLE OF INVENTION: THEM.
FILE REFERENCE: 11000.1073
CURRENT APPLICATION UNBERS: US/10/650,274
CURRENT FILING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 187
SOFTWARE: FASISEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 91
LENGTH: 426
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                                                                                          VB-10-343-6504-660

Sequence 660, Application US/10343650A

Sequence 660, Application US/10343650A

GENERAL INFORMATION:
APPLICANT: HAGA, TATSUVA

TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REPERBYCE: 31671-186347

CURRENT APPLICATION NUMBER: US/10/343,650A

CURRENT FILING DATE: 2003-07-21

PRIOR APPLICATION NUMBER: JP 2001/33418

PRIOR APPLICATION NUMBER: JP 2001/34434

PRIOR PILING DATE: 2001-02-13

PRIOR FILING DATE: 2001-02-13

SOFTWARE: PATENTIN Ver: 2.1

SEQ ID NO 660

LENGTH: 343

TYPE: PRT

CREANISM: Homo sapiens

US-10-343-650A-660
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Pred. No. 25;
9; Mismatches
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299 NLRGOSKTFSNVČELMEFS 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.1%;
Best Local Similarity 33.3%;
Matches 11; Conservative s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GLENN, MATTHEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Sequence 50060, Application US/10425114A

Sequence 50060, Application US/10425114A

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Acvalic, David K.
APPLICANT: Acvalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
TILE REFERENCE: 38-21 (5313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 50060
LENGTH: 458
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                          Gaps
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                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 23.9%; Score 48.5; DB 6; Length 458; Best Local Similarity 37.1%; Pred. No. 40; Matches 13; Conservative 7; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 6; Length 335;
Pred. No. 34;
8; Mismatches 14; Indels
                        12; Indels
                                                                                           370 GSARFFSPLGVYDFVKRTQFIQYSAAAL--ATQADAIVTLAQT 410
                                                                5 GSRRVFS-----KKCRLVKFSMVALVSATMAVTTVTLENT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3592-069-B11_FLI.pep
US-10-425-114A-50060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 RYFEKDWDMVSFIRSLKAMVRSSNSVAVVTFPSTVLS 230
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OTHER INFORMATION: Clone ID: 700423405_FLI.pep

US-10-425-114A-62521
Best Local Similarity 37.2%; Pred. No. 32; Matches 16; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 62521, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaeka, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 35.1%;
Matches 13; Conservative
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ORGANISM: Zea mays
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ORGANISM: Zea mays
                                                                                                                                                                      RESULT 14
US-10-425-114A-50060
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January 5, 2004, 13:53:52; Search time 3240 Seconds (without alignments) 11085.300 Million cell updates/sec
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1083
1 GACAACGCCTTCTTTTTCT......TGTGCAAAAAGCAAAAAGC 1083
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                 33363688 segs, 16581889874 residues
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Maximum Match 100%
Listing first 45 summaries
                                 OM nucleic - nucleic search, using sw model
                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                     Title:
Perfect score:
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/ptodata/2/pna/US101B COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 1, Appli
ID	9 US-08-482-785-7	US-09-119-900-7	US-10-453-032-7	US-08-188-721-1
DB	6	16	23	9
% Query Match Length DB	1083	1083	1083	1021
% Query Match	100.0	100.0	100.0	88.8
Score	1 1083 100.0 1083 9	1083	1083	961.6
Result No.	н	7	٣	4

us-08-482-785-7.rnpm

APPLICATION NUMBER: US/08/393,889 FILING DATE: 24-FEB-1995 FILING DATE: US/08/082,845 FILING DATE: US/08/082,845 FILING DATE: US/08/082,845 ATTORNEY/AGENT INFORMATION: NAME: Farber, Michael B. REGISTRATION NUMBER: 32,612 REFERENCE/DOCKET NUMBER: 9521 TELEPHONE: (818) 796-4000 TELEPAX: (818) 795-6321 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 1083 base pairs TYPE: nucleic acid STRANDEDNESS: double TYPE: DAA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO ONIGINAL SOURCE: ORGANISM: Streptococcus pyogenes FEATURE: NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS	Query Match 100.0%; Score 1083; DB 9; Length 1083; Best Local Similarity 100.0%; Pred. No. 3e-239; ndels 0; Gaps 0; Matches 1083; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 61 TATTGATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Db 121 ACAGCAIATGATCTACTGGATCAAGACGGGTTTTTTTTTT
Sequence 1, Appli Sequence 11, Appl Sequence 11, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 11740, Appl Sequence 113, Appl Sequence 113, Appl Sequence 113, Appl Sequence 113, Appl Sequence 1145, Appl Sequence 1145, Appl Sequence 1145, Appl Sequence 1145, Appl Sequence 1145, Appl Sequence 11740, Appl Sequence 1145, Appl Sequence 117445, Appl Sequence 11744, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli	Sequence 49678, A Sequence 974, App Sequence 974, App Sequence 34579, A Sequence 4430, App Sequence 4200, Ap Sequence 16, App Sequence 259, App Sequence 359, App Sequence 359, App Sequence 366, App Sequence 366, App Sequence 366, App Sequence 366, App Sequence 366, App Sequence 359, App Sequence 359, App Sequence 359, App Sequence 359, App Sequence 359, App Sequence 359, App Sequence 369	Sequence
6 US-08-188-721A-1 9 US-08-188-721A-1 16 US-09-119-900-11 53 US-10-453-032-11 9 US-08-482-785-14 9 US-08-482-785-14 9 US-08-119-900-14 9 US-08-119-900-14 9 US-08-119-900-10 53 US-10-453-032-10 9 US-09-119-900-10 53 US-10-453-032-12 24 US-09-119-90-12 25 US-09-119-90-12 26 US-09-119-90-132 27 US-09-119-90-132 28 US-09-806-708B-22 29 US-09-806-708B-22 20 US-09-806-708B-22 21 US-09-806-708B-22 22 US-09-806-708B-22 23 US-09-806-708B-22 24 US-09-806-708B-22 25 US-09-806-708B-22 26 US-10-257-166-113 27 US-08-466-194-14 28 US-10-257-166-113 29 US-08-466-194-14 50 US-10-257-166-113 20 US-08-466-194-14	US-09-8119-091h-49678 US-09-534-859-974 US-09-803-736-974 US-09-110-279-89 US-09-710-279-489 US-09-710-279-4430 US-09-710-279-4200 US-09-710-279-4200 US-09-710-279-4200 US-09-710-279-459 US-00-710-279-459 US-00-21-613-16 US-00-046-933-366 US-60-066-933-366 US-00-066-933-366 US-00-066-933-366 US-00-066-933-366 US-00-068-228-369	ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS THE 82-785-7 THERE 1 INFORMATION: APPLICANT: Adms, Craig W. APPLICANT: Pang, Party PY. APPLICANT: Pang, Party PY. APPLICANT: Belei, Marina TITLE OF INVENTION: Streptococcus pyogenes NUMBER OF SEQUENCES: 16 CORRESPONDENCES: 16 CORRESPONDENCES: 16 CORRESPONDENCES: 16 CORRESPONDENCES: 16 CORRESPONDENCES: 16 CORRESPONDENCES: 16 CORRESPONDENCES: 16 CORRESPONDENCES: 16 CORRESPONDENCES: 16 CORRESPONDENCES: 16 CORRESPONDENCES: 16 CORPUTRY: USA STREET: 225 South Lake Avenue, Ninth Floor CITY: Peasdena STATE: California CONTRY: USA ZIP: 91001 COMPUTER: Floppy disk COMPUTER: Floppy disk COMPUTER: Floppy disk COMPUTER: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/482,785 FILING DATE: 07-JUN-1995 CLASSIFICATION DATA:
	1014 62927 62927 2403 2406 2946 2946 3350 6013 11178 15892 15892 15892 15892	4.0 744802 49 US-10 ication US/08482785 dams, Craig W. eng, Marina NYION: Streptococcus NYION: Streptococcus NYION: Streptococcus Sheldon & Mak Sheldon & Mak Gena if fornia is FORM: i: Flopy disk i:
99996 99222 99222 092222 09222 09222 09222 09222 09222 09222 09222 09222 092222 092222 092222 092222 09222 09222 09222 09222 09222 09222 09222 09222 09222 09222 09222 09222 09222 09222 09222 09222 09222 0922	य य य य य य य य य य य य य य य य	ESULT 1 Sequence 7, Application US/08482785 GENERAL INFORMATION: APPLICANT: Adams, Craig W. APPLICANT: Belei, Maxina TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Recombinant TITLE OF INVENTION: APPLICANT CORRESPONDENCE ADDRESS: ADDRESSE: Shaldon & Mak STREET: California COUNTRY: USA ZIP: 91001 COMPUTER: IBM PC COMPATION MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION SOFTWARE: PARABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION SOFTWARE: PARABLE FORM: APPLICATION NUMBER: US/08/482 FILING DATE: APPLICATION DATA: APPLICATION DATA:
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540 099 720 840 121 ACAAGCATATGAATCTACTTGGATCAAGACGGGTTTTTTCTAAAAAATGTCGGCTAGTAA 180 241 ATACTGCACTGGCACGACAAACACACGCTCTCAAATGATGTTGTTCTAAATGATGCGCAA 300 301 GCAAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAA 360 CTTTAGGTACTAGTCAGATTACTCCCAGCACTCTTTCCTAAAGCAGGAGATATTCTCTATA 420 540 900 900 9 720 780 780 ACAAGCATATGAATCTACTTGGATCAAGACGGGTTTTTTTCTAAAAAATGTCGGCTAGTAA 180 AATTTTCAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAA 240 241 ATACTGCACTGGCACGACAAACACAGGTCTCAAATGATGTTGTTCTAAATGATGGCGCAA 300 301 GCAAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAA 360 CITTAGGIACTAGICAGAITACICCAGCACICTITCCIAAAGCAGAGAIAITCICIAIA 420 GCAAATTAGATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATG 480 9

Query Match 100.0%; Score 1083; DB 53; Length 1083; Best Local Similarity 100.0%; Pred. No. 3e-239; Animilarity 100.0%; Pred. No. 3e-239; Matches 1083; Conservative 0; Mismatches 0; Conservative 0; Qy 1 GACAACGCCTTCTTTTTCTCCTTACTACTACTCCTTTAATTTTCATATTTTTAAAAAA	Qy 121 ACAAGCATATGAATCTACTTGGATCAAGACGGGTTTTTTTCTAAAAAATGTCGGCTAGTAA 180	Qy 181 AATTITCAATGGTTGTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAA 240	Qy 241 ATACTGCACTGGCACAAACACAGGTCTCAAATGATGTTGTTCTAAATGATGGGGCAA 300 	OY 301 GCAACTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAA 360	Qy 361 CTTTAGGTACTAGTCAGATTACTCCAGCACTCTTTCCTAAAGCAGGAGATATTCTCTATA 420	OY 421 GCAAATTAGATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATG 480	Qy 481 TTGAAGGTACGGTGTTAGACAATCTTTCGGTAAAAATCAAAACCCCGCAGGATGGA 540	Qy 541 CTGGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCG 600	Qy 601 GAGATTTCTGGAATAGAAGTCATCTCATTGCAGATAGTCTCGGTGGAGATGCACTCAAGA 660 -	Qy 661 TCAATGCCGTTACAGGAACACGTACCCAAAATGTAGGAGGTCGTGACCAAAAAGGCGGCA 720 	Qy 721 TGCGCTATACCGAACAAAGAGCTCAAGAATGGTTAGAAGCAAATCGTGATGGCTATCTT 780	Qy 781 ATTATGAAGTCGCTCCAATCTACAACGAGACGAGTTGATTCCAAGAGCTGTCGTGGTAT 840	Qy 841 CAATGCAATCTTCTGATAATACCATCAAGGAAAGTATTAGTTTACAACACAGGTAATG 900 	Qy 901 GCTACACCATTAACTACCATAACGGTACACCTACTCAAAATAACCAAAAGGCTAGAC 960	Qy 961 CTCTGCTCACTAGGCCTAGCTTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAAA 1020
Qy 841 CAATGCAATCTTCTGATAATACCATCAACGAGAAAGTATTAGTTTACAACACAGCTAATG 900 Db 841 CAATGCAATCTTCTGATAATACCATCAACGAGAAAGTATTAGTTTACAACACACAC	Qy 1021 TACTAGAAAAGCAATGATTGCCGTCATTGTTTTATGAATTTGTGCAAAAAGCAAAAA 1080 Db 1021 TACTAGAAAAAGCAATGATTGCTTTTTTATGAATTTGTGCAAAAAGCAAAAA 1080	Oy 1081 AGC 1083 Db 1081 AGC 1083	RESULT 3 US-10-453-032-7	; Sequence ', Application US/10453032; GENERAL INFORMATION: APPLICANT: Adams, Craig W. APPLICANT: Pang, Patty PY.) APPLICANT: Belel, Marina ; TITLE OF INVENTION: Recombinant DNase B Derived from ; TITLE OF INVENTION: Streptococcus pyogenes ; NUMBER OF SEQUENCES: 16	CORRESPONDENCE ADDRESS: ADDRESSES: Sheldon & Mak STREET: 225 South Lake Avenue, Ninth Floor CITY: Pasadena	Cal C: C	MEDIUM TIFE: Floppy disk MEDIUM TIFE: Floppy disk COMPUTER: Decemberable COMPUTER: Patentin Release #1.0, Version #1.25	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/453,032 FILING DATE: 03-UNE-2003 CLASSIFICATION:	# PAPLICATION NUMBER: US/08/082,845 # TILING DATE: 23-JUNE-1993 # ATTORNEY/AGRY INVERMITON:	OCKET NOTION IN		pase c aci dou near	Z ; 5) OKGANISM: Streptococcus pyogenes ; FATURE: ; NAME/KEY: CDS ; LOCATION: 129944 US-10-453-032-7

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                                                                                      147 ACAAGCATATGAATCTACTTGGATCAAGACGGGTTTTTTCTAAAAAATGTCGGCTAGTGA
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US-08-188-721A-1
Sequence 1, Application US/08188721A
GENERAL INFORMATION:
APPLICANT: Yuteudo, Takashi
APPLICANT: Wemaski, Makoto
APPLICANT: Hara, Ayako
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                                                                                                                                                                                                                  APPLICANT: TURBUGO, TAKABAIL
APPLICANT: TURBUGO, TAKABAIL
APPLICANT: Hasa, Ayako
APPLICANT: Hasa, Ayako
APPLICANT: Hasa, Ayako
APPLICANT: Hasa, Masamichi
APPLICANT: Takeda, Yoshifumi
APPLICANT: Takeda, Yoshifumi
APPLICANT: Takeda, Yoshifumi
APPLICANT: Hinuma, Yorio
TITLE OF INVENTION: Method of Microdetection Therefor
NUMBER OF SEQUENCES:
ADDRESSE: Birch, Stewart, Kolasch & Birch
STREET: Bill Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 31-JAM-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 43.2
ATTORNEY, AGENT INFORMATION:
NAME: MULFDY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFREENCE/POCKET NUMBER: 1422-178P
TELECOMMUNICATION INFORMATION:
TELEFHONE: (703) 205-8050
TELEFAX: (703) 205-8050
TELEFAX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1021 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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ORGANISM: Streptococcus pyogenes
STRAIN: NY-5
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                                                                                                                                                                                                          Yutsudo, Takashi
Okumura, Koichi
                                                                AGC 1083
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ANTI-SENSE: N
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; LOCATION:
US-08-188-721-1
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US-08-188-721-1
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APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
APLICANT: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ZIP: 91001
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       APPLICANT: Kishishita, Masamichi
APPLICANT: Takeda, Yoshifumi
APPLICANT: Takeda, Yoshifumi
APPLICANT: Igarashi, Hisanaga
APPLICANT: Hinuma, Yorio
TITLE OF INVENTION: Mitogenic Factor, Gene Thereof and
TITLE OF INVENTION: Method of Microdetection Therefor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                              CONDITAT: 0.5.4.

CID: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,721A
FLING DATE: 31.-24N-1994
FLIANG DATE: 31.-24N-1994
FLIANG PATE TATAON NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1422-178P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEETAX: (703) 205-8000
TELEETAX: (703) 205-8000
TELEETAX: (703) 205-8000
TELEETAX: 243345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10.21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
MODECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

88.8%; Score 961.6; DB 6;
Best Local Similarity 98.5%; Pred. No. 3.1e-211;
Matches 981; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptococcus pyogenes STRAIN: NY-5
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155..967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-08-188-721A-1
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CTGCTCACTAGGCCTAGCTTTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAATA 1022
                                                                                                                       661 TATGAAGTCGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGGTATCA 720
                                                                                                                                                                                                    903 TACACCATTAACTACCATAACGGTACACCTACTCAAAAATAATACCAAAAGGCTAGACCT 962
                                                                                                                                                                                                                                                                                                                                                                                   841 CTGCTCACTAGGCCTAGCTTTTTACATCAAAAAAAGCAATGACTATAGAAAGTAAAAATA 900
                                                 601 CGCTATACCGAACAAAGAGCTCAAGAATGGTTAGAAGCAAATCGTGATGGCTATCTTTAT 660
                                                                                                                                                                               843 ATGCAATCTTCTGATAATACCATCAACGAGAAAGTATTAGTTTACAACACAGCTAATGGC 902
                                                                                                                                                                                                                                                                                              781 TACACCATTAACTACCATAACGGTACACCTACTCAAAAATAATACCAAAAGGCTAGACCT
                                                                                            783 TATGAAGTCGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09119900
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OFFICIAL STATES STATES SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                              1023 CTAGAAAAGCAATGATTGCCGTCATTGC 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901 CTAGAAAAGCAATGATTGCCGTCATTGC 929
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CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/082,845
APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FATDER, MICHAEL B.
REGISTATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPAN: (818) 795-4000
TELEPAN: (818) 795-401

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
'TEMMETH: 940 base pairs
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 795-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.6%;
Matches 925; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 940 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCGGA 602
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                                                                                                                  TITICAAIGGIAGCICTIGIAICAGCCACAAIGGCIGIAACAACACICACACTIGAAAAI 242
                                                                                                                                    TTTTCAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAAAT 120
                                                                                                                                                                      ACTGCACTGGCACGACAAACACAGGTCTCAAATGATGTTGTTCTAAATGATGGCGCAAGC 302
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                                                                                          1 Argearcceaarcracrrcearcaaeaceeerrrrrrrrraaaaarerceecraeraaa
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                                                                 Gaps
                                       o;
                Length 940;
             Score 922.6; DB 16; Length
Pred. No. 3e-202;
0; Mismatches 4; Indels
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             85.2%;
99.6%;
               Query Match
Best Local Similarity 99.6
Matches 925; Conservative
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RESULT 8 US-10-453-032-11 ; Sequence 11, Application US/10453032

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APPLICANT: Pang, Patty P. Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 AUDRESSEE: Sheldon & Mak STREET: 225 South Lake Avenue, Ninth Ploor CITY: Pasadena STATE: California CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ILING DATE: 23-UNE-193
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (818) 796-4000 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,032
FILING DATE: 03-JUNE-2003 ORGANISM: Streptococcus pyogenes (genomic) TELEFAN. (818) 795-6321 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 940 base pairs TYPE: nucleic acid STRANDEDNESS: double Matches 925; Conservative MOLECULE TYPE: DNA Query Match Best Local Similarity USA ANTI-SENSE: NO ORIGINAL SOURCE US-10-453-032-11 COUNTRY: 183 61 303 181 363 423 d à

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TATGAAGTCGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGGTATCA 842
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MAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 795-400
TELEFAX: (818) 795-431
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 937 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECITE
                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptococcus pyogenes
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Best Local Similarity 95.7'
Matches 889; Conservative
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US-08-482-785-14
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                                               GAAGGTAGCTACGGTGTTAGACAATCTTTCGGTAAAAATCAAAACCCCGCAGGATGGACT
                                                                                                                           GGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCGGA
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Sequence 14, Application US/08482785

GENERAL INFORMATION:
FAPPLICANT: Pang, Patty P.-Y.
APPLICANT: Belel, Marina
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
NUMBER OF SEQUENCES: 16
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STREE: California
STREET: California
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785
FILING DATE: 07-40N-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: US/08/082,845
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAGAAAAGCAATGATTGCCGTCATTGC 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                         1 ArgeArccGAAccrGcrGcrrccGrGrTrTrcrccCAAAAAATGCCGTCTGGTTAAA
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              Mismatches
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          Conservative
        Matches 889;
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658 TATGAAGTCGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGGTATCA
                                                     903 TACACCATTAACTACCATAACGGTACACCTACTCAAAAATAATACCAAAAGGCTAGACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 853.8; DB 16;
Pred. No. 2.3e-186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 225 South Lake Avenue, Ninth Floor
CITY: Passadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                          CTAGAAAAGCAATGATTGCCGTCATTGC 1051
                                                                                                                                                                                                                                                              APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase
TITLE OF INVENTION: Streptococcus pyog
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION VINDER: 32,612
REFERRICE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEFAX: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09119900 GENERAL INFORMATION:
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95.7%;
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                             US-09-119-900-14
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; LOCATION;
US-09-119-900-14
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APPLICANT: Adams, Patty P.-Y.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: POPPOW disk
COMPUTER: PROPERTION: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UN-U995
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
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APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: US/08/082,845
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-482-785-10
Sequence 10, Application US/08482785
GENERAL INFORMATION:
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TITLE OF INVENTION: Recombinant DNase B Derived from TITLE OF INVENTION: Streptococcus pyogenes NUMBER OF SECURDINGES: 16 CORRESPONDENCE ADDRESS: SHeldon & Man. STREET: 225 6-100 Mar.
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                                                                                                                                                                                                                                                                                                            COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-JUNE-2003
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 853.8; DB 53
Pred. No. 2.3e-186;
0; Mismatches 37;
                                                                                                                                                                                             STREET: 225 South Lake Avenue, Ninth Floor CITY: Pasadena STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/082,845
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ORIGINAL SOURCE;
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,84
FILING DATE: 23-JUNE-1993
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELECAM: (818) 795-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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95.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 937 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.7
Matches 889; Conservative
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; LOCATION:
US-10-453-032-14
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ORGANISM: Streptococcus pyogenes
US-09-119-900-10
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           REFERENCE/DOCKET NUMBER: 952:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                          1 GACAACGCCTTCTTT
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CITY: Pasadena
STATE: California
COUNTRY: USA
ZIP: 91001
                                                                                                                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                         18.5%; Score 200; DB 9; Length 200; 100.0%; Pred. No. 1.2e-35; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-110-900-10

Sequence 10, Application US/09119900

GENERAL INFORMATION

APPLICANT: Madem, Craig W.

APPLICANT: Pang, Patty P.-Y.

APPLICANT: Belei, Marina

TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS: 3

ADDRESSES: Sheldon & Mak

STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Pasadena STATE: California COUNTRY: Pasadena STATE: California COUNTRY: USA STATE: California CONPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Streptococcus pyogenes
US-08-482-785-10
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                 NAME: Farber, Michael B.
REGISTRATION NUMBER: 32.612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEFAN: (818) 795-4000
TELEFAX: (818) 795-4101
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDENESS: double
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                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
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ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.C
Matches 200; Conservative
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CLASSIFICATION:
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             Length 200;
                                                       Indels
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GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P. Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,032
FILING DATE: 03-JUNE-2003
Ouery Match
18.5%; Score 200; DB 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 200; Conservative 0; Mismatches 0;
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225 South Lake Avenue, Ninth Floor
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: 23-UNE-1993
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REGISTRATION NUMBER: 9521
TELECOMMUNICATION:
TELEPHONE: (818) 795-4000
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                                                                                                                                                                                                                                                                                         Length 200;
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US-08-482-785-12
i Sequence 12, Application US/08482785
i GENERAL INFORMATION:
    APPLICANT: Pang, Patty P.-Y.
    APPLICANT: Belai, Marina
    TITLE OF INVENTION: Recombinant DNase B Derived from
    TITLE OF INVENTION: Recombinant DNase B Derived from
    TITLE OF INVENTION: Streptococcue pyogenes
    NUMBER OF SEQUENCES: 16
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Sheldon & Mak
    STREET: 225 South Lake Avenue, Ninth Floor
    CITY: Pasadena
    STATE: California
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTONN WUMBER: US/08/082,845
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ATTONN WUMBER: US/08/082,845
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ATTONN WUMBER: US/08/082,845
FILING DATE:
ATTONN WUMBER: US/08/082,845
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ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/POCKET NUMBER: 9521
FELECHMUNICATION INFORMATION:
TELEPHONE: (818) 795-4000
TELEFAX: (818) 795-6321
TELEFAX: (818) 795-6321
INFORMATION FOR SEG ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 200; Conservative
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                                                                                                                                                                                                                                                                                                                                  Length 182;
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Best Local Similarity 77.3%; Pred. No. 4.3e-14;
Matches 143; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: January 5, 2004, 16:40:20 Job time : 3248 secs
                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                        ) ORGANISM: Synthetic primer
US-08-482-785-12
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 CAAGC 182
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ORGANISM: Streptococcus pyogenes FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
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Sequence 12, Appl
Sequence 12, Appl
Sequence 15, Appl
Sequence 39, Appl
Sequence 31, Appl
Sequence 117, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 115, Appl
Sequence 115, Appl
Sequence 115, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 175, Appl
Sequence 175, Appl
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                                                                                                                                                                                                                                                                                                                       1083
1 GACAACGCCTTCTTTTTTCT......TGTGCAAAAAGCAAAAAGC 1083
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Sequence
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Sequence
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-472-630-11
US-08-472-630-14
US-08-472-630-12
US-08-472-630-12
US-10-221-714A-151
US-10-394-948-31
US-10-313-793-39
US-10-31-793-39
US-10-21-714A-417
US-10-433-793-108
US-10-433-793-108
US-10-64-025-2813
US-10-64-025-2813
US-10-221-714A-814
US-10-221-714A-814
US-10-221-714A-499
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US-10-221-714A-499
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US-10-231-714A-69
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Maximum Match 100%
Listing Eirst 45 summaries
                                                                                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                       Perfect score:
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Sequence 19015, A Sequence 296, App Sequence 520, App Sequence 121, App Sequence 6919, App Sequence 6919, App Sequence 19179, App Sequence 194, App Sequence 194, App Sequence 196, App Sequence 1980, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 2356, App Sequence 199, Appl
        Sequence Sequence S
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US-60-500-337-191533
US-60-500-337-19155
US-10-473-126-296
US-10-221-714A-520
US-10-433-793-121
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US-60-519-270-2355
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ALIGNMENTS

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Sequence 7, Application US/08472630
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
Ang, Patty P.-Y.
Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION: «Unknown»
PRIOR APPLICATION ON THE STATEMENT OF THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT ON THE STATEMENT OF THE STATEMENT ON THE STATEMENT ON THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATE
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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STATE: California
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      CTCTGCTCACTAGGCCTAGCTTTTACATCAAAAAAAGCAATGACTATAGAAAGTAAAAA
                                                                      1021 TACTAGAAAAAGCAATGATTGCCGTCATTGCTTTTTTATGAATTTTGTGCAAAAAGCAAAAA
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                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Recombinant DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.2%; Score 922.6; DB 4;
llarity 99.6%; Pred. No. 2.4e-267;
Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pyogenes
NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: CURKNOWNS
ATTORNEY/AGENT INFORMATION:
NAME: FAIDER, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (818) 796-4000 (ELEFAX: (818) 795-6321
                                                                                                                                                                                                                                                  Sequence 11, Application US/08472630
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
Pang, Patty P.-Y.
Belei, Marina
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SEQUENCE DESCRIPTION: SEQ ID
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 91001
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCES:
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Matches 925; Conserv
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                                                                           Query Match
100.0%; Score 1083;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1083; Conservative 0; Mismatches
               LOCATION: 129..944
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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NAME/KEY:
                                            US-08-472-630-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AAATTAGATGAGTTAGGAAGGACGCGTACTAGCTAGAGGTACATTGACTTATGCCAATGTT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 AAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 GGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATGTTATGTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 AAGCATATGAATCTACTTGGATCAAGACGGGTTTTTTTCTAAAAATGTCGGCTAGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Arggarccgaaccrgcrggrrcccgrcgrgrrrrcrccaaaaaagccgrcrggraaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 TTTTCAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 ACTGCACTGGCACGACAAACACGGTCTCAAATGATGTTGTTCTAAATGATGGCGCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ACCGCTCTGGC---TCAGACACAGGTCTCAAATGATGTTGTTCTAAATGATGGCGCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 AAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATTAGATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGGTAGCTACGGTGTTAGACAATCTTTCGGTAAAAATCAAAAACCCCGCAGGATGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 GAAGGTACCGACGTTAGACAATCTTTCGGTAAAAATCAAAAACCCCGCAGGATGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTAGGTACTAGTCAGATTACTCCAGCACTCTTTCCTAAAGCAGGAGATATTCTCTATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 937;
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRITY APPLICATION DATE:
APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 78.8%; Score 853.8; DB 4; Best Local Similarity 95.7%; Pred. No. 1.2e-246; Matches 889; Conservative 0; Mismatches 37;
                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 1..819
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-472-630-14
                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 795-4000
TELEPHONE: (818) 795-6321
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 937 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
    California
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
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                                                                     ACTGCACTGGCACGACAAACACAGGTCTCAAATGATGTTGTTATTAAATGATGGCGCAAGC 180
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                                                                                                                              AAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAACT 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              720
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TITICAATGGTAGCTCTTGTATCAGCCACAATGGCTGTAACAACAGTCACACTTGAAAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGCAATCTTCTGATAATACCATCAACGAGAAAGTATTAGTTTACAACACAGCTAATGGC 902
                                                                                                                                                      181 AAGTACCTAAACGAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAACT
                                                                                                                                                                                                                                                                                                    AAATTAGATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATGTT
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                                          ACTGCACTGGCACGACAAACACAGGTCTCAAATGATGTTGTTCTAAATGATGGCGCAAGC
                                                                                                                                                                                                                 TIAGGTACTAGTCAGATTACTCCAGCACTCTTTCCTAAAGCAGGAGATATTCTCTATAGC
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes
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GENERAL INFORMATION:
APPLICANT: Radms, Craig W.
Pang, Patty P.-Y.
Belei, Marina
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US-08-472-630-14
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
Pang, Patty P.-Y.
Belei, Marina
TITLE OF INVENTION: Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AATTTTCAATGGTAGCTCTT 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
                               LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
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SEQUENCE CHARACTERISTICS:
LENGTH: 182 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.58
Best Local Similarity 100.0
Matches 200, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                  AATGCCGTTACAGGAACACGTACCCAAAATGTAGGAGGTCGTGACCAAAAAGGCGGCATG 722
                                                                                                                                                                                                                                           CGCTATACCGAACAAGAGCTCAAGAATGGTTAGAAGCAAATCGTGATGGCTATCTTTAT 782
                                                                                                                                                                                                                                                                                                                                                                    842
GGAAACCCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCGGA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          838 CIGCICACTAGGCCTAGCITITITACATCAAAAAAGCAATGACTATAGAAAGTAAAAATA 897
                                                                                                                            478 GATTICTGGAATAGAAGTCATCTCATTGCAGATAGTCTCGGTGGAGATGCACTCAGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           783 TATGAAGTCGCTCCAATCTACAACGCAGGTGGAGTTGATTCCAAGAGCTGTCGTGGTATCA
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STRET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
OOFFWARE: PATON NOATA:
APPLICATION NOATA:
FILING DATE: 07-Jun-1995
CLASSIFICATION DATA:
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes
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APPLICATION NUMBER: US/08/082,845
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: FAIDES, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1023 CTAGAAAAGCAATGATTGCCGTCATTGC 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         898 CTAGAAAAGCAATGATTGCCGTCATTGC 926
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GENERAL INFORMATION:
APPLICANT: Adamm, Craig W.
Pang, Patty P.-Y.
Belei, Marina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FELEFAX: (818) 795-6321
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SEQUENCE CHARACTERISTICS
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US-08-472-630-10
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                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION: <unbox/cunknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: <unbox/cunknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sheldon & Mak
STRET: 225 South Lake Avenue, Ninth Floor
TIY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                  18.5%; Score 200; DB 4;
100.0%; Pred. No. 4.9e-50;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
SEQUENCE DESCRIPTION: SEQ ID NO: 10;
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us-08-482-785-7.rnpn

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5289 AAAATTAACTAAAAAATACGACAAAAAATCTTATTTTTCTCCCCTATTTACACTAATT 5230
                                                                                                                                                                                                                                              3169 CTAATCAAAACAAATATA-TTCATAAATTAAATTTATAAATACAAATAAAATAAAAAA 5111
                                                                                                                                           5229 TITITITACTAAAATAAAACCAAAAAATITCITAATITCIAATITAAATITAATTACAAACIT 5170
                                                                                        TITICIAAAAAATGICGGCTAGTAAAATTTTCAATGGTAGCTCTTGTATCAGCCACAATG 215
                                                                                                                                                                                                 216 GCTGTAACAACAGTCACACTTGAAAATACTGCACTGGCACGACAAACACAGGTCTCAAAT 275
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                                                                                                                                                                                                                                                                                                             276 GATGTTGTTCTAAATGATGGCGCAAGCAAGTACCTAAACGAAGCATTAGCTTGGACATTC 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/10433793
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/433,793
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 39
LENGTH: 7503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   924 GGTACACCTACTCAAAAATAATACCAAAAGGCTAGACCTCTGCTCACTAGGCCTAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            984 TTACATCAAAAAAGCAATGACTATAGAAAGTAAAAATACTAGAAAAAGCAA 1035
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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Novel Compositions and Methods in Cancer TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 5.2942000900
CURRENT APPLICATION NUMBER: US/10/394,948
CURRENT APPLICATION NUMBER: US/10/394,948
CURRENT APPLICATION NUMBER: US/10/394,948
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/367,025
PRIOR APPLICATION NUMBER: US 60/367,025
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 167163
TYPE: DNA
CRGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42.4; DB 7; Length 7503; Pred. No. 0.062; 0; Mismatches 81; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5050 AAAATAATCTCTAATCTTTAAAAATCT 5024
                                                                                                                                                                                                                                                                                                                                                                                                                        336 AATGACAGTCCTAACTATTACAAACT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.9%;
Matches 91; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-433-793-39/c
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US-10-394-948-31/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGGCAATGGATCCGAACCTGCTTCCCGTCGTCTTTTCTCCAAAAAAGCCGTCTGG 60
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                                                                                                                                                                                                                                                                             Score 106.6; DB 4; Length 182;
Pred. No. 6.2e-22;
0; Mismatches 39; Indels 3
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4.3%; Score 46.2; DB 7; Length 6106;
Best Local Similarity 48.3%; Pred. No. 0.0041;
Matches 158; Conservative 0; Mismatches 168; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Lumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT FILING DATE: 2000-03-12
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR PELICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-06
PRIOR PELICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
                                                                                                                                                                 ORGANISM: Synthetic primer
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Sequence 151, Application US/10221714A
; GENERAL INFORMATION:
                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
STRANDEDNESS: single
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Best Local Similarity 77.3%;
Matches 143; Conservative
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ORGANISM: Artificial Sequence
                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
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Score 40.8;
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Best Local Similarity 50.5%;
Matches 100; Conservative (
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                 LENGTH: 37184
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                     131 GAATCTACTTGGATCAAGACGGGTTTTTTCTAAAAAATGTCGGCTAGTAAAATTTTCAAT 190
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                                                                                                                                                                                              911 TAACTACCATAACGGTACACCTACTCAAAATAATAACACAAAAGGCTAGACCTCTGCTCAC 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1036 raarcccaacacrirraaaaaaccaaaaraaaraaarcaccraaaaarcaaaarrcaaaac 977
                                                                                                                                                                                                                                                                                  71 CTAGTTAAGTAAGCGTATACTTAGTTAGCGAAATTAGAAAAGAGGACAAAT
                                                                                                                                                              0; Gaps
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                                                                                                            Score 42.4; DB 7; Length 167163;
Pred. No. 0.22;
0; Mismatches 106; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OLEK, ALEXANDER

APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Lumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137236 AGIGTTTATCGTATCATAAACACTGTTCTAA 137205
                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 GGTAGCTCTTGTATCAGCCACAATGGCTGTAA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 417, Application US/10221714A GENERAL INFORMATION:
                    ; LOCATION: (1) ... (167163)
; OTHER INFORMATION: n = A,T,C or G
US-10-394-948-31
                                                                                                        Query Match
Best Local Similarity 50.0%;
Matches 106; Conservative
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Best Local Similarity 52.6
Matches 90; Conservative
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NAME/KEY: misc_feature
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LENGTH: 5413
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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/433,793
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DIEENBROCK, Christian
APPLICANT: DIEENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Metabolism
FILE REFERENCE: 5013.1010
CURRENT APPLICATION NUMBER: US/10/240,454A
CURRENT APPLICATION NUMBER: DC10-04-06
PRIOR APPLICATION NUMBER: DC10-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR PLICATION NUMBER: DE 10019173.8
PRIOR PLICATION NUMBER: DE 10019173.8
PRIOR PLICATION NUMBER: DE 100132529.7
PRIOR APPLICATION NUMBER: DE 1004366.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 68
LENGTH: 8238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41.2; DB 7; Length 37184; Pred. No. 0.28; 0; Mismatches 98; Indels 0;
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DB 7; Length 8238;

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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
FITLE OF INVENTION: proliferative disorders
FITLE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 150
LENGTH: 3814
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OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER PIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT APPLICATION NUMBER: US/60/487,610
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NOS: 97101
SOFTWARE: FASELSEQ for Windows Version 4.0
TURNETH: 133801
TYPE: NAW
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48.2%; Pred. No. 1.1;
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                                     0
        42 YYWYWRAMKRRWMWRKWRSWSWMWMAWGMTRWAARMWRWY
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3.7%; Score 40; DB 7;
Best Local Similarity 51.7%; Pred. No. 0.25;
Matches 91; Conservative 0; Mismatches 85
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                                                                                                                                                                           Sequence 150, Application US/10473126 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Matches 109; Conservative
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ORGANISM: Homo sapiens
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US-60-487-610-19911/c
                                                                                                                       RESULT 13
US-10-473-126-150/c
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                                                                                     856 ATAATACCATCAACGAGAAAGTATTAGTTTACAACACAGCTAATGGCTACACCATTAACT 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTACTAGTCAGATTACTCCAGCACTCTTTCCTAAAGCAGGAGATATTCTCTATAGCAAA 425
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                                       Gaps
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                                     Indels
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(US-10-664-025-2813/Application US/10664025

(GENERAL INFORMATION:
) APPLICANT: Unumes Minne Edwards, J.B.
) APPLICANT: Glorano, J.Y.
) TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2
) CURRENT APPLICATION NUMBER: US/09/621,976
) PRIOR APPLICATION NUMBER: US/09/621,976
) PRIOR APPLICATION NUMBER: US/09/621,976
) NUMBER OF SEQ ID NOS: 19335
) SOFTWARE: Patent.pm
) SEQ ID NO 2813
                                     87;
     llarity 51.7%; Pred. No. 0.2; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
Best Local Similarity
Matches 93; Conserv
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; LOCATION: 235..399
US-10-664-025-2813
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                                                                                                                             335 CAATGACAGTCCTAACTATTACAAACTTTAGGTACTAGTCAGATTACTCCAGCACTCTT 394
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                                                                                                                                                                                                                                                                                                                                                                               50362 raaaaaaaagaaarccarrrrcaarrrcgracragaaacrcagra 50317
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                                                                                                                                                                                                                                                                                                 395 TCCTAAAGCAGGAGATATTCTCTATAGCAAATTAGATGAGTTAGGA 440
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Sequence 324.7

Sequence 324.4

Sequence 324.7

Sequence 324.7

Sequence 324.7

September 3124.7

September 3124.7

APPLICANT: OLEK, Alexander

APPLICANT: PIEPEMBROCK, Christian

APPLICANT: BERLIN, Kurt

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: tumor suppressor genes and oncogenes

FILE REFERENCE: 3013.1005

CURRENT APPLICATION NUMBER: US/10/221,714A

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: DE 10013847.0

PRIOR FILING DATE: 2000-03-15

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 1001382529.7

PRIOR APPLICATION NUMBER: DE 100335229.7

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 100335229.7

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Search completed: January 5, 2004, 17:31:06 Job time : 3038 secs

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Minimum DB Maximum DB

Database

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Sequence 5038, Ap
Sequence 7751, Ap
Sequence 3636, Ap
Sequence 4, Appli
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Sequence 288, App
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Sequence 2698, App
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GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Screptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CITY: Pagadena
STATE: California
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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length: 2000000000
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Match Length DB
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Score

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APPLICATION NUMBER: US/08/082,845 FILING DATE:
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PRIOR APPLICATION NUMBER: US/08/082,845
FILING DATE: 23-UNRE-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOWUNICATION INFORMATION:
TELEPAN: (818) 796-4000
INFORMATION SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/10453032 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1:00.
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MEDIUM TYPE: Floppy disk
                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-09-119-900-8
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 VTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, marina
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1418; DB 8;
100.0%; Pred. No. 5.8e-144;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 SSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
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CITY: Pasadena
STATE: California
STATE: USA
ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
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                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: US/08/082,845
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                            NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 795-6321
INFORMATION FOR SEQ ID NO: 8:
SEQUIENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09119900 GENERAL INFORMATION:
07-JUN-1995
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.'
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-482-785-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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181 VTGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQ 240
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                                                                                                                                    1 MILLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY
                                                                     Gaps
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   DB 15; Length 271;
                                                                  Indels
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APPLICANT: Pang, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Bellei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PALLCATION NUMBER: US/10/453,032
FILING DATE: 03-JUNE-2003
Query Match 100.0%; Score 1418; DB 15; Best Local Similarity 100.0%; Pred. No. 5.8e-144; Matches 271; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 225 South Lake Avenue, Ninth Floor CITY: Pasadena STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 SSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
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REFERENCE/DOCKET NUMBER: 1422-178P
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                                                                                                                                                                                                                                                                                         Length 271;
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APPLICANT: Yutsudo, Takashi
APPLICANT: Lwasaki, Makoto
APPLICANT: Hwaski, Makoto
APPLICANT: Hashita, Masamichi
APPLICANT: Takeda, Yoshifumi
APPLICANT: Takeda, Yoshifumi
APPLICANT: Igarashi, Hisanaga
APPLICANT: Igarashi, Hisanaga
APPLICANT: Hinuma, Yorio
TITLE OF INVENTION: Mathod of Microdetection Therefor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch c--
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,721A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: MATCHY JF., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                     100.0%; Score 1418; DB 30;
100.0%; Pred. No. 5.8e-144;
tive 0; Mismatches 0;
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APPLICANT: Yutsudo, Takashi
NAME: Farber, Michael B.
REGIETRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 795-4300
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 anino acids
                                                                                                                                                                                                                                                                                                                          Matches 271; Conservative
                                                                                                                                                                                                                      / MOLECULE TYPE: protein
US-10-453-032-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                            linear
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US-08-188-721A-2
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61 LINEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEG 120
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APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        Score 1411; DB 5;
Pred. No. 3.3e-143;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
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APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/482,785
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-482-785-15; Sequence 15, Application US/08482785; GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: FAIDER: Michael B.
RESISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.3%;
Matches 269; Conservative
                                                                                                                                                     LENGTH: 271 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-188-721A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 225 South I
CITY: Pasadena
STATE: California
COUNTRY: USA
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63 NEALAWTENDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 TGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 YGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNAV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 TGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS 241
                                                                                                                                                                                                                                                                                                                                                              62 NEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGS 121
                                                                                                                                                                                                                                                                 2 NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYL 61
                                                                                                                                                                                                                                                                                                             4 NLIGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALA-QTQVSNDVVLNDGASKYL 62
                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                    Query Match 98.6%; Score 1397.5; DB 15; Length 272; Best Local Similarity 99.6%; Pred. No. 9.7e-142; Matches 269; Conservative 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/10453032
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDNTINEKVLVYNTANGYTINYHNGTFTQK 272
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FILING DATE: 03-UNB-2003
CLASSIFICATION: 03-UNB-2003
APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: 23-UNB-1993
ATTORNEY/AGENT INFORMATION:
NAME: FATAPE, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (818) 796-4000
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 272 amino acids
TYPE: amino acid
TOPOLOGY: linear
       SEQUENCE CHARACTERISTICS
                                                                                               MOLECULE TYPE: protein US-09-119-900-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                TYPE: amino acid
TOPOLOGY: linear
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                               LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                 4 NLIGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALA-QTQVSNDVVLNDGASKYL 62
                                                                                                                                                                                                                                                                                                                                                      2 NLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYL 61
                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                            98.6%; Score 1397.5; DB 8; Length 272; 99.6%; Pred. No. 9.7e-142; tive 0; Mismatches 0; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEB: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDNTINEKVLVYNTANGYTINYHNGTPTOK 271
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 15, Application US/09119900
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FATDER, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/POCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                   TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-5321
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acids
TOPOLOGY: linear
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.6
Matches 269; Conservative
                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-482-785-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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ORGANISM: Streptococcus pyogenes
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMINICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS LENGTH: 229 amino aci
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 California
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225 Sout
CITY: Pasadena
STATE: Californ
  ORIGINAL SOURCE
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ZIP: 91001
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US-09-119-900-9
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                                                                                                                                                                                                                                                                                                                                                          TCTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS 242
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                                                                                                                                                                                                                                                                                                                                                                                                                        182 TGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS 241
                                                                                                                                                                                                                                            62 NEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGS 121
                                                                                                                                                       2 NILGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYL 61
                                                                                                                                                                                4 NLIGSRRVESKKCRLVKFSMVALVSATMAVTTVTLENTALA-QTQVSNDVVLNDGASKYL 62
                                                                                                                1; Gaps
                                                                  Score 1397.5; DB 30; Length 272; Pred. No. 9.7e-142; 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Adams, Craig W.
APPLICANT: Pang, Party P.-Y.
APPLICANT: Pang, Party P.-Y.
APPLICANT: Realei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CHENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-482-785-9; Sequence 9, Application US/08482785; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 95.
TELECOMMUNICATION:
TELEPHONE: (818) 796-4000
                                                                Query Match
Best Local Similarity 99.6%;
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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  protein
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STATE: California
COUNTRY: USA
MOLECULE TYPE:
      , MOLECULE TY1
US-10-453-032-15
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43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 102
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                                                                                                                                                                                                                                                                                                                                           163 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 222
                                                                                                                                                                                                                                                                                                                                                                             121 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 180
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                                                            Gaps
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Query Match 86.0%; Score 1220; DB 8; Length 229; Best Local Similarity 100.0%; Pred. No. 1.2e-122; Matches 229; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09119900
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
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225 South Lake Avenue, Ninth Floor
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
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1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDB 60
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                                                                                                                                  LGRIRTARGILIYANVEGSYGVRQSFGKNQNPAGWIGNPNHVKYKIEWLNGLSYVGDFWN 162
                                                                                                                                                                                                         RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 222
                                                                                           1 RÓTQVSNDVVINDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 60
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                                                            43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
                       Gaps
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                                                                                                                                                                                                                                                                                                         PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
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                       Indels
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Sequence 9, Application US/10453032
Sequence 9, Application US/10453032
Sequence 9, Applications
APPLICANT: Adms, Craig W.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATCHING SYSTEM:
COMPUTER: BATCHING SYSTEM:
COMPUTER: BATCHING SOFTWARE:
SACTHARE: PACHICATION DATA:
APPLICATION NUMBER: US/10/453,032
FILING DATE: 03-JUNE-2003
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 23-JUNE-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

86.0%; Score 1220; DB 30;
Best Local Similarity 100.0%; Pred. No. 1.2e-122;
Matches 229; Conservative 0; Mismatches 0;
   100.0%; Pred. No. 1.2e-122; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 95.
TELECOMMUNICATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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   al Similarity 100.
229; Conservative
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
: USA
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STATE: Californ
COUNTRY: USA
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                                                                                                                                    103
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     Best Local
Matches 22
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Sequence 263, Application US/10360101
; GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way
TITLE OF INVENTION: Export 105/10/360,101
CURRENT APPLICATION NUMBER: EP 02077060.8
FRICH APPLICATION NUMBER: EP 02077060.8
FRICH REPER PROBLEM 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.1
SEQ ID NO 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 RVYKGQGTSEKRVTVSDVVYNPLDGYKRSTGAYGVVTKDMIDMSKGYREKWETNPEPSGW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 FRFYNRADNEEISEKEYDSRRTKSYKVTNNVPVVLTTLKGKKYNSHLFVASHLFADSLGG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AGDILYSKLDELGRTRTARGTLTYANVEGSYGVRQSFGKNONPAGW 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 -----TGN----TGN-----PNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 DALRVNAVTGTRTONVGGRDOKGGMRYTEORAOEWLEANRDGYLYYEVAPIYNADELIPR 233
7 NIVLAKTVSVNQ-------TYGEYKDYYTVIGESNIDQSAFPKIYKTTE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 NTALARQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPK----
                                                                                                                                                                                                                                   181 PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.2%; Score 371; DB 29; Length 303; Best Local Similarity 32.6%; Pred. No. 1.3e-30; Matches 89; Conservative 36; Mismatches 84; Indels 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08482785
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from TITLE OF INVENTION: Streptococcus pyogenes
NUMBR OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 AVVVSMQSSDNTINEKVLVYNTANGYTINYHNG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 SVLVSALSSDGVINETVRVFNTADGFNINYEKG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: sequence of streptodornase US-10-360-101-263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10453032
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Matina
TITLE OF INVENTION: Recombinant DNage B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Peadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,032
FILLING DATE: 03-JUNE-2003
CLASSIFICATION STREET
PRIOR APPLICATION NUMBER: US/06/082,845
FILLING DATE: 23-JUNE-1993
ATTONNEY/AGENT INFORMATION:
NAME: FRIEDET MINER: 32,612
REGISTRATION NUMBER: 32,612
REGISTRATION NUMBER: 32,612
            PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHORE: (818) 795-400
TELEFAX: (818) 795-410
TELEFAX: (818) 795-410
TELEFAX: (818) 795-410
TELEFAX: (818) 795-410
TELEFAX: (818) 795-410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                          LENGTH: 43 amino acids
TYPE: amino acid
TOPOLGY: innear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO:
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LENGTH: 43 amino acids
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
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GENERAL INFORMATION:
APPLICANT: Adams. Craig W.
APPLICANT: Belei, Marina
ITILE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDESS:
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
                                                                                                                                   COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785
FILING DATE: 07-JUN-1995
CLASSIFICATION: AJS-5
FILING DATE: 24-FEB-1995
FILING DATE: 24-FEB-1995
FILING DATE: 324-FEB-1995
FILING DATE: 324-FEB-1995
APPLICATION NUMBER: US/08/082,845
FILING DATE: 325-612
REGISTRATION NUMBER: 32,612
REGISTRATION NUMBER: 32,612
REGISTRATION NUMBER: 32,612
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: (818) 796-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LUMBUTH: 43 maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
14.3%; Score 203; DB 8; I
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 43; Conservative 0; Mismatches 0;
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                CITY: Pasadena
STATE: California
COUNTRY: USA
ZIP: 91001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-482-785-1
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Sequence 7.80-0

Sequence 7.80-0

Sequence 7.80-0

APPLICANT: Adams, Craig W.
APPLICANT: Balei, Marina
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF INVENTION: Streptococcus pyogenes
TITLE OF INVENTION: Apple 8

CORRESPONDENCE ADDRESS:
ADDRESSES: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CONDUTRY: USA

CONDUTRY: USA

ZIP: 9100A

ZIP: 9100A

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                                                                                                                                                                                                                                                                                                                                                                                                         1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
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Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 38; Conservative 0; Mismatches 0;
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HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
US-08-482-785-6
                                                                                                                                                  ORGANISM: Streptococcus pyogenes US-10-453-032-1
                                                                         N-terminal
   peptide
MOLECULE TYPE: pe
HYPOTHETICAL: NO
FRAGMENT TYPE: N-
ORIGINAL SOURCE:
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US-08-482-785-6
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Search completed: January 5, 2004, 18:55:06 Job time : 325.403 secs

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Sequence 8, Appli
Sequence 15, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 436, Appli
Sequence 4092, Appli
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                                                                                                                                                                                                                                                                                                                   1 MNLLGSRRVFSKKCRLVKFS......VYNTANGYTINYHNGTPTQK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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Sequence 8
Sequence 1
Sequence 2
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Sequence 6
Sequence 5
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7: /cgn2_6/ptodata/2/paa/USO8_NEW COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-472-630-16

US-08-472-630-16

PCT-USO3-27401-436

US-10-472-928-4092

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US-10-425-114A-69718
US-10-425-114A-53765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        320769 segs, 64697744 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                           January 5, 2004, 18:39:19
                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
                                                                                                                                                                                                                                                              US-08-482-785-8
1418
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                           Run on:
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27 86.5 6.1 566 6 US-10-425-114A-47841 Sequence 28 86.5 6.1 1709 7 US-6-490-1897 Sequence 28 86.5 6.1 1709 7 US-6-490-1897 Sequence 28 86.5 6.1 1709 7 US-6-490-1897 Sequence 28 86.5 6.1 1709 7 US-6-490-1897 Sequence 28 86.5 6.0 1485 19.5 ES-0.0597-5.66.19 Sequence 29 84.5 6.0 1485 19.5 ES-0.0597-5.66.19 Sequence 29 84.5 6.0 1485 19.5 ES-0.0597-5.66.19 Sequence 29 84.5 6.0 1486 19.5 ES-0.0597-5.66.19 Sequence 29 84.5 6.0 1486 19.5 ES-0.0597-5.66.19 Sequence 29 84.5 6.0 1486 19.5 ES-0.0597-5.66.19 Sequence 29 84.5 6.0 1486 19.5 ES-0.0597-5.66.19 Sequence 29 84.5 6.0 1486 19.5 ES-0.0597-5.66.19 Sequence 29 84.5 ES-0.0597-5.0597-5.66 19.5 ES-0.0597-5.69 19.5 ES-0.0597-5.69 19.5 ES-	47841, A 1987, Ap 11, Appl 15, Appl 6199, Appl 34, Appl 13, Appl 13, Appl 13, Appl 14, Appl 164, Appl 164, Appl 164, Appl 164, Appl 164, Appl 164, Appl 164, Appl 17, Appl 17, Appl 17, Appl 17, Appl 17, Appl 17, Appl 18, Appl 18, Appl 19, Appl 19, Appl 10,		Gaps 0;
27 86.5 6.1 566 6 US-10-425-114A-47841 28 66.5 6.1 1391 6 US-10-67-046-13 30 86 6.1 1391 6 US-10-67-046-13 31 85.5 6.0 482 5 US-08-70-67-046-13 32 85.5 6.0 482 5 US-08-70-67-046-13 33 85.5 6.0 1435 6 US-10-67-046-13 34 84.5 6.0 1436 6 US-10-41-16-79 35 83.5 9 355 1 US-08-70-9183-164 36 83.5 9 355 6 US-10-41-16-79 36 83.5 9 355 6 US-10-41-16-79 37 83.5 9 355 1 PCT-US03-1573-25 40 83 5.9 1203 6 US-10-437-30-164 38 83.5 9 1203 6 US-10-437-30-164 39 83 5.9 1203 6 US-10-437-30-164 39 83 5.9 1203 6 US-10-437-31-31-164 30 8.5 9 1203 6 US-10-437-31-164 30 8.5 9 1203 6 US-10-437-31-164 31 8.5 9 1203 6 US-10-437-31-164 32 5.9 1203 6 US-10-437-31-164 32 5.9 1203 6 US-10-437-31-164 33 5.9 1203 6 US-10-437-31-164 34 82.5 9 1203 6 US-10-437-31-164 35 5.9 1203 6 US-10-437-31-164 36 5.9 1203 6 US-10-437-31-164 37 12 12 12 12 12 12 12 12 12 12 12 12 12	edinence edi		,17
28 66.5 6.1 566 6 US-10-42E-114A-4 28 66.5 6.1 1799 7 US-6-190-990-180-180-180-180-180-180-180-180-180-18	Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა 	##1	Length Indels
	86.5 6.1 566 6 US-10-425-114A-47 86.5 6.1 1709 7 US-60-490-890-198 9 86 6.1 1391 6 US-10-687-046-11 1 85.5 6.0 482 5 US-9897-516A-61 2 84.5 6.0 1475 1 PCT-0803-06962-34 3 6.0 1475 1 PCT-0803-06962-34 4 6.0 1436 US-10-687-046-13 8 6.0 1436 US-10-687-046-13 8 6.0 5635 6 US-10-687-046-13 8 3.5 9 US-10-687-046-13 8 3.5 9 US-10-687-046-13 8 3.5 9 US-10-687-046-13 8 3.5 9 US-10-61-168-78 8 3.5 9 US-10-61-168-78 8 3.5 9 US-10-61-72-164-73 9 3.5 9 US-10-61-72-164-73 <t< td=""><td>SULT 1 SULT 1 SEQUENCE 8, Application US/08472630 GENERAL INFORMATION: PAIGH CORRESPONDENCE ADDRESS: 16 CORRESPONDENCE ADDRESS: 8 ADDRESSEE: Sheldon & MAK STREET: 225 South Lake Avenue, Nint CITY: Pasadena STATE: California COUNTRY: USA ZIP: 91001 COMPUTRY: USA ZIP: 91001 COMPUTRY: BER PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATCHION ACCOMPAIGH APPLICATION NUMBER: US/08/472,630 FILING DATE: 07-Unn-1995 CLASSIFICATION NUMBER: US/08/472,630 FILING DATE: UNKNOWN> PRIOR APPLICATION NUMBER: US/08/082,845 FILING DATE: UNKNOWN> PROSTIFICATION NUMBER: 32,612 REGISTRATION NUMBER: 32</td><td>/ Match Local Similarity 100.0%; Pred. No. 6e-106; nes 271; Conservative 0; Mismatches 0</td></t<>	SULT 1 SULT 1 SEQUENCE 8, Application US/08472630 GENERAL INFORMATION: PAIGH CORRESPONDENCE ADDRESS: 16 CORRESPONDENCE ADDRESS: 8 ADDRESSEE: Sheldon & MAK STREET: 225 South Lake Avenue, Nint CITY: Pasadena STATE: California COUNTRY: USA ZIP: 91001 COMPUTRY: USA ZIP: 91001 COMPUTRY: BER PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATCHION ACCOMPAIGH APPLICATION NUMBER: US/08/472,630 FILING DATE: 07-Unn-1995 CLASSIFICATION NUMBER: US/08/472,630 FILING DATE: UNKNOWN> PRIOR APPLICATION NUMBER: US/08/082,845 FILING DATE: UNKNOWN> PROSTIFICATION NUMBER: 32,612 REGISTRATION NUMBER: 32	/ Match Local Similarity 100.0%; Pred. No. 6e-106; nes 271; Conservative 0; Mismatches 0

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TGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS 242
                                                                                YGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNAV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQTTPALFPKAGDILYSKLDE
                                                                                                               123 YGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGBALRVNAV
NEALAWTFNDSPNYYKTLGTSQ1TPALFPKAGD1LYSKLDELGRTRTARGTLTYANVEGS
                                                                                                                                                                     TGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQS
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COMPUTER: IBM PC compatible
CORENTER: Batentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT ABLICATION DATA:
APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION: vUnknown>
PRIOR APPLICATION OTHER: US/08/082,845
FILING DATE: vUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: Farber: wichael B.
REGISTRATION NUMBER: 32,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Adams, Craig W.
Pang, Party P.-Y.
Balei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.0%; Score 1220; DB 4;
llarity 100.0%; Pred. No. 3.1e-90;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes
                                                                                                                                                                                                                                                          SDNTINEKVLVYNTANGYTINYHNGTPTOK 271
                                                                                                                                                                                                                                                                                                SDNTINEKVLVYNTANGYTINYHNGTPTOK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptococcus pyogenes
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION IRFORMATION:
TELEPHONE: (818) 795-4000
TELEFAX: (818) 795-6321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHRARACTERISTICS:
LENGTH: 229 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08472630 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Pasadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE
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Best Local Simi
Matches 229;
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                                                                                     61 INEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEG 120
                                                                                                                                                   SYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSLGGDALRVNA 180
                                                                                                                                                                                VTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQ 240
                                                                                                                                                                                                                                                               LNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEG 120
                    1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITAL TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION INMBER: US/08/082,845
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: US/08/082,845
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Recombinant DNase B Derived from Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.6%; Score 1397.5; DB 4 99.6%; Pred. No. 2.6e-104; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                           241 SSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
                                                                                                                                                                                                                                                                                                                                                    SSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Farber, Michael B. REGISTRATION NUMBER: 32,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-08-472-630-15
US-08-472-630-15
Sequence 15, Application US/08472630
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adams, Craig W.
Pang, Patty P.-Y.
Belei, Marina
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SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEOUENCES:
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US-08-472-630-16
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US-08-472-630-6
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                                           LGRITRIARGILIYANVEGSYGVRQSFGKNQNPAGWIGNPNHVKYKIEWINGLSYVGDFWN 120
                                                                                                                                   LGRIRTARGILIYANVEGSYGVRQSFGKNONPAGWIGNPNHVKYKIEWLNGLSYVGDFWN 162
                                                                                                          RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                         181 PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 229
                                                                                                                                                                                             223 PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION NUMBER: US/08/082,845
FILING DATE: CURKNOWN>
APPLICATION NUMBER: US/08/082,845
FILING DATE: CURKNOWN>
ATORNEY/AGENT INFORMATION:
NAME: Fazber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Recombinant DNase B Derived from Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNLLGSRRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALAR 43
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ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08472630
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
Pang, Patty P.-Y.
Belei, Marina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (818) 795-6321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 43 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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Matches 43; Conservative
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                  103
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ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
CITY: Dasadena
CITY: USA
COUNTY: USA
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION: CURNOWn>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 38;
                                     APPLICANT: Adams, Craig W.
APPLICANT: Adams, Party P.-Y.
Balei, Marina
TITLE OF INVENTION: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08472630
GENERAL INFORMATION:
GENERAL INFORMATION:
Pang, Party P.-Y.
Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 ROTOVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 80
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14.2%; Score 202; DB 4; Best Local Similarity 100.0%; Pred. No. 7.8e-10; Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: «UNKNOWN-
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pyogenes
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 6:
Sequence 6, Application US/08472630 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                           NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Pasadena
STATE: California
COUNTRY: USA
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RESULT

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130 KNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSL-----GGDALR----VNAV 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 TTVTLENTALARQTQVSNDVVLNDGASKYLNEALAWTFND
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8.9%; Score 126.5; DB 6;
Best Local Similarity 21.9%; Pred. No. 0.0061;
Matches 59; Conservative 37; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SSDNTINEKVLVYNTANGYTINYHNGTPT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 SSDGELEFNVLVPNVOKGLOLDYRTGEVT 271
                                                                                                                                                                                      241 SSDNTINEKVLVYNTANGYTINYHNGTPT 269
                                                                                                                                                                                                               243 SSDGELEFNVLVPNVQKGLQLDYRTGEVT 271
                                                                                                                                                                                                                                                                                                                                         Sequence 4092, Application US/10472928 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08472630
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
Pang, Patty P.-Y.
Belei, Marina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMAT:
US-10-472-928-4092
                                                                                                                                                                                                                                                                                                                           US-10-472-928-4092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TUFTS UNIVERSITY
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS, TREATMENT AND
TITLE OF INVENTION: PREVENTION OF ACTIVE INFECTION
TITLE OF INVENTION: PREVENTION OF ACTIVE INFECTION
FILE REFERENCE: 700355-5294-612
CURRENT APPLICATION NUMBER: PCT/US03/27401
CURRENT FILING DATE: 2003-09-02
PRIOR PILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 560
SOFTHARE: PARENTIN VETSION 3,2
SEQ ID NO 436
LENGTH: 274
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                                                                             COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
FILING DATE: 07-Jun-1995
FILING DATE: UNKNOWN>
PRIOR APPLICATION NUMBER: US/08/082,845
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 32,612
TELEFAX: (818) 796-4000
TELEFAX: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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8.9%; Score 126.5; DB 1;
Best Local Similarity 21.9%; Pred. No. 0.0061;
Matches 59; Conservative 37; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
12.0%; Score 170; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 32; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptococcus pyogenes
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US03-27401-436; Sequence 436, Application PC/TUS0327401; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Streptococcus pneumoniae PCT-US03-27401-436
                       ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-472-630-16
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11; 182 IGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQ 240 72 SPNYYKTLGTSQITPALFPKAGDILYSKLDE--LGRTRTARGTLTYANVEGSYGVRQSFG 129 130 KNONPAGWIGNPNHVKYKIEWLNGLSYVGDFWNRSHLIADSL-----GGDALR---VNAV 181 182 IGTRIQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQ 240 37 TNLSOKKQASEAPSQALAESVLTDAVKSQIKGSLEWNGSGAFIVNGNKTNLDAKVSSKPY APPLICANT: CHERON SpA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: TEREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: PO26926W0
CURRENT PPLICATION NUMBER: US/10/472,928
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 4092 OTHER INFORMATION: DNA-entry nuclease (enda)
OTHER INFORMATION: Cellular location: outside
OTHER INFORMATION: Similar to strain R6 sequence 15903821 (e-156) 97 ADNKTKTVGKETV----PTVANALLSKATRQYKNRKETGNGSTSW-----

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APPLICANT: Zhou, Yillous
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
FURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
   12;
                                                                                                                                                                                  216
                                                                                                           115 YANVEGSYGVRQSFGKNQNPAG------WTGNPNHVKYKIEWLNGLSYVG-----DF 160
                                                                                                                                                                                                         56 GASKYLNEALAWTFNDSPNYYKTL-GTSQITPALFPKAGDILYSKLDELGRTRTARGTLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 LIADSLGGDALRVNAVTGTRTQN-----VGGRDQ-----KGGMRYTEQRAQEWLE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ROSFGK-----NONPAGWTGNPNHVKYKIEWLNGLSYVGDFWNRSH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 DIADNWG-----SMTSRADQNDRWASYAGPGGWNDPDMLEVGNGGMSEAEYRS---- 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 ANRDGYLYYEVAPIYNADELIPRAV-VVSMQSSDNTINEKVLVYNT----ANGYTINYHN 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 -----HFSIWALAKAPLLIGCDVRAMSQQTMGILSNSEVIAVNQDSQGAQGKKVQSSN 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 NTALAROTQVSNDVVLNDGASK----YLNEALAWTFNDSPNYYKTLGTSQITPALFPKAG 93
                                                                                                                                 51 -FNVTHSYGLTETFG----PASICTWKPEWDNLPQDAQAKLKARQGVAHVGMEGLDVKDP
                                                          6 GAPTVLNMII----NSSPKVQKPLPGKVQVMTGGAPPPPDVIF-RMEELG------
                                                                                                                                                                                  161 WNRSHLIAD--SLGGDALRVNAVTGTRTQNVGGRDQ--KGGMRYTEQRAQEWLEANRDGY
   26;
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   Indels
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                                                                                                                                                                                                                                                                                 | | | : ::: | : ::::
|----ELKDRSKDIIISGGENISTIELEGVIFS 190
                                                                                                                                                                                                                                                        217 LYYEVAPIYNADELIPRA--VVVSMQSSDNTINEKVLVYN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: UC-ZMFLMO17008E12_FLI.pep
US-10-425-114A-57900
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 57900, Application US/10425114A GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
   39;
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   Conservative
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Best Local Similarity
Matches 62; Congerv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                          162 I-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 G 266
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LENGTH: 446
   51;
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   Matches
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Pred. No. 1.4;
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                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                  STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%; Score 106; DB 4;
95.7%; Pred. No. 0.021;
tive 0; Mismatches
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: «Unknown»
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                               APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pyogenes SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                             NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51758, Application US/10425114A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (818) 796-4000
                                                                                    ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                     (818) 795-6321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS
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                                                  STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.77
Best Local 22; Conservative
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Best Local Similarity
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US-10-425-114A-51758
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SEO ID NO 26323
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APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO S6379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Clone ID: UC-ZMFLB73183G03_FLI.pep
US-10-425-114A-56379
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; GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Stater, Thomas M.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Seq:
TITLE OF INVENTION: Xenorhabdus sp. Genome Seq:
TILE REFERENCE: 38-21(51847)B
CURRENT FILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: US/09/897,516A
CURRENT FILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: US 60/215,161
FRIOR APPLICATION NUMBER: US 60/215,161
FRIOR APPLICATION NUMBER: US 60/215,161
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FRIOR APPLICATION NUMBER: US 60/215,161
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                              Sequence 56379, Application US/10425114A GENERAL INFORMATION:
                                                                                                               APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 20.69
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
US-10-425-114A-56379
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US-09-897-516A-6933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HORDNITTORIAPD---PIKEPNGISGVASKVHALGLKFGIYSDAGINTCAGYPGSYGYEA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 IDAQAFSDWGVDYLKYDNCNNLGLAGNATISSKRYKRMGDALKNVSRPIFFSLCSWGTDD 194
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                                                                                                                                                                                                                                                                                                                255
                                                                                                                                                                                                                                                                                                                                                                267 RSRPYLF-----SNSLAPSIVAASIKVLDMLKDGDELRERLWRNANLFREKM----T 314
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                                                                                                                                                                                                                                    213 HAVGFVGKHGRGTHEYCDVMG----RVDIITGTLGKALGG--ASGGYTAARKEVVEWLRQ
                                                                                                                                                                                                152 NGLSYVGDFWNRSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEA
                                                                                                                                                                                                                                                                                                                   212 NRDGYLYYEVAPIYNADELIPRAVVVSMQSSD-------NTINEKVLVYNT
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                                                                                                                                       34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.3%; Score 89; DB 6; Length 396; Best Local Similarity 20.9%; Pred. No. 8.7; Matches 68; Conservative 39; Mismatches 136; Indels 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26323 Application US/10679063
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054) B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT PILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER: OF SEQ ID NOS: 27373
                                                                                 Length 398;
                                                                                                                                       Indels
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                                                                                 ch 6.3%; Score 90; DB E
1 Similarity 24.6%; Pred. No. 7.3;
31; Conservative 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Umbelopsis vinacea
US-10-679-063-26323
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ORGANISM: Xenorhabdus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |:|:
315 AAGFTL 320
                                                                                    Query Match
Best Local Similarity
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                           US-09-897-516A-6933
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127 SFGKNON------PAGWTGNPNHVKYKIEWLNGLSYVGDFWNRS------HLIA 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 RRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKYLNEALA 66
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS, TREATMENT AND TITLE OF INVENTION: PREVENTION OF ACTIVE INFECTION FILE REFERENCE: 700355-2541-PCT CURRENT APPLICATION NUMBER: PCT/US03/27401 CURRENT FILING DATE: 2003-09-02 PRIOR PILILIATION NUMBER: US 60/407,082 PRIOR FILING DATE: 2002-08-30 NUMBER OF SEQ ID NOS: 560 SGCTWARE: Patentin version 3.2 SEQ ID NO 377 LENGTH: 646
                                                                                                                                                                                                                                                                                                                                                      Query Match 6.2%; Score 88; DB 1; Length 646;
Best Local Similarity 21.6%; Pred. No. 17;
Matches 75; Conservative 42; Mismatches 83; Indels 148; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 LIPRAVVSMQSSDNTINEKVLVY-NTANGY-------TINY 263
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                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
PCT-US03-27401-377
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Appli Appli Appl

Scoring table:

Perfect score:

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Seguence:

Minimum DB seq Maximum DB seq

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Sequence 263, App Sequence 6, Appli Sequence 6, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 21, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 3631, App Sequence 3634, App Sequence 4, Appli Sequence 4, Appli Sequence 2698, App Sequence 2698, App Sequence 2698, App Sequence 2698, App Sequence 80, Appl Sequence 81, Appl Sequence 2698, App Sequence 2698, App Sequence 80, Appl Sequence 81, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 82, App
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Sequence 359, App
                                                        Sequence 8, App
Sequence 8, Ap
Sequence 15, Ap
Sequence 15, A
Sequence 15, A
Sequence 15, A
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GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Streptococcus pyogenes
ITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STRET: 225 South Lake Avenue, Ninth Floor
CITY: Peadena
STATE: California
5. US-09-119-900-9
10. US-10-433-032-9
10. US-08-422-785-8
11. US-08-119-900-8
11. US-08-422-785-8
12. US-09-119-900-8
13. US-08-115-900-15
14. US-08-482-785-8
15. US-09-119-900-15
16. US-08-482-785-16
17. US-08-482-785-16
18. US-08-482-785-16
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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179.5
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                                                                   Sequence 9, Appli
                                                                                                                                                                                             ; Search time 273.282 Seconds (without alignments) 762.478 Million cell updates/sec
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1 RQTQVSNDVVLNDGASKYLN......vynTanGYTINYHNGTPTQK 229
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| cgn2_6/ptodata/2/paa/NCTCOMB.pep:*
| cgn2_6/ptodata/2/paa/USOG_COMB.pep:*
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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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                                                                                                                                                                                                   January
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Score

Regult No.

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61 LGRTRTARGTLTYANVEGSYGVRQSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1220; DB 15; Length 229; 100.0%; Pred. No. 1.9e-122; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Adams, Craig W.
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Bellei, Marina
APPLICANT: Bellei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUCRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,032
FILING DATE: 03-JUNE-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: 23-JUNE-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICAL
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE DOCKET NUMBER: 9521
TELECHONE: (818) 796-400
TELEPHONE: (818) 796-400
TELEPHONE: (818) 796-401
INFORMATION FOR SEG ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/10453032 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 229; Conservative
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                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
SOFTWARE: PatentI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LGRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Bang, Patty P.-Y.
APPLICANT: Bang, Patty P.-Y.
APPLICANT: Bang, Patty P.-Y.
APPLICANT: Bang, Patty P.-Y.
APPLICANT: Bang, Patty P.-Y.
APPLICANT: Bang, Patty P.-Y.
APPLICANT: Bracken Streptococcus pyogenes
ITTLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREE: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1220; DB 8; Best Local Similarity 100.0%; Pred. No. 1.9e-122; Matches 229; Conservative 0; Mismatches 0;
       FILING DALE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: US/08/082,845
FILING DATE: NICORATION:
NAME: Falber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 796-4000
TELEFAX: (818) 796-4000
TELEFAX: (818) 796-4000
TELEFAX: (818) 796-4000
TELEFAX: (818) 796-4000
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TELEFAX: (818) 796-4000
TELEFAX: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-119-900-9
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INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 271 amino acidatore.
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TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                 LENGTH: 271 amino acids;
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: protein
US-08-482-785-8
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ADDRESSEE: Sheldon &
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 60
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                                                                                                                                                                                                                                                                                                                                                 Length 229;
                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785
FLING DATE: 07-JUN-1995
CLASSIFICATION 135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: US/08/082,845
FILING DATE: US/08/082,845
                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1220; DB 30; Best Local Similarity 100.0%; Pred. No. 1.9e-122; Matches 229; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                         ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08482785 GENERAL INFORMATION:
                  REFERENCE/DOCKET NUMBER: 9521
                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 795-6321
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 mmino acide
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 225 South L
CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 91001
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43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 102
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                                                                                                                                                                                                                                                                61 LGRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 222
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Query Match 100.0%; Score 1220; DB 8; Length 271; Best Local Similarity 100.0%; Pred. No. 2.4e-122; Matches 229; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09119900
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P. Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER FEADMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPEDATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: FRADER: MINER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION NUMBER: 9521
TELECOMMUNICATION NUMBER: 9521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
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45 QTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDEL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 GRIRIARGILIYANVEGSYGVRQSFGKNONPAGWIGNPNHVKYKIEWLNGLSYVGDFWNR 164
                                                                              RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 SHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAP 181
                                   103 LGRIRIARGILIYANVEGSYGVRQSFGKNONPAGWIGNPNHVKYKIEWLNGLSYVGDFWN 162
                                                                                                                      163 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 222
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                                                                                                                                                                                         PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 271
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                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/08482785
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.6%; Score 1215; DB 8; L 100.0%; Pred. No. 8.5e-122; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 225 South Lake Avenue, Ninth Floor CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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amino acid
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.
Matches 228; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                           43 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 102
                                                                                                                                                                     LGRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 120
                                                                                                                                                                                                                103 LGRIRTARGILIYANVEGSYGVROSFGKNONPAGWIGNPHVKYKIEWLNGLSYVGDFWN 162
                                                                                  1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 60
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Length 271;
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                                        Indels
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GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
100.0%; Score 1220; DB 15;
100.0%; Pred. No. 2.4e-122;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PALLCATION NUMBER: US/10/453,032
FILING DATE: 03-JUNE-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1220; DB 30;
Pred. No. 2.4e-122;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: 23-UNE-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Scc.
100.0%; Pre
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sheldon & Mak
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acids
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Matches 229; Conservative
                 Best Local Similarity 100.
Matches 229; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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US-10-453-032-8
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  Query Match
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165 SHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAP 224
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                                                                                      225 IYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 272
                                                             182 IYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 1215; DB 15; Length 272; 100.0%; Pred. No. 8.5e-122; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 IYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTOK 229
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                                                                                                                                                                                                                                APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Streptococcue pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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Justing Progress:
STREET: 25.5 South Lake Avenue, Ninth Floor STATE: California COUNTRY: USA ZIP: 91001
COMPUTE: 91001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPAN: (818) 795-6321
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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Matches 228; Conservative
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45 QTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDEL 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWNR
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                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,032
FILING DATE: 03-JUNE-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.6%; Score 1215; DB 30;
100.0%; Pred. No. 8.5e-122;
tive 0; Mismatches 0;
                                                                                                                                                                 NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
ADDRESSEE: Sheldon & Mak
CITY: Pagadena
Sequence 15, Application US/10453032
GENERAL INFORMATION:
APPLICANT: Pang, Patry P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDER:
APPLICATION UNDER:
SPILING DATE: 23-JUNE-1993
ATTORNEY/AGENT INFORMATION:
NAME: FALACE, MICHAEL B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMUNICATION INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Yutsudo, Takashi
APPLICANT: Okumura, Koichi
APPLICANT: Iwasaki, Makoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-10-453-032-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Iwasaki, Mal
APPLICANT: Hara, Ayako
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                        STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                          ZIP: 91001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-08-188-721A-2
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--PNH 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 RAQEWLEANRDGYLYYEVAPIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINY 221
                                                                                                                                                                                                                                                                                                                                                            26 TFNDSPNYYKTLGTSQITPALFPK------AGDILYSKLDELGRTR
                                                                                                                                                                                                                        Length 303;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08482785
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Bang, Patty P.-Y.
APPLICANT: Belei, Martina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,785
FILING DATE: O7-UM-1995
CLASSIFICATION 35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,889
FILING DATE: 24-FRB-1995
APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                        Query Match 29.9%; Score 365; DB 29; Best Local Similarity 34.6%; Pred. No. 5.5e-30; Matches 84; Conservative 34; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                             66 TARGILIYANVEGSYGVROSFGKNONPAGW-----TGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
                                                                                                                                                ; OTHER INFORMATION: sequence of streptodornase US-10-360-101-263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Farber, Michael B. REGISTRATION NUMBER: 32,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
  SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 HNG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 EKG 259
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                    SEQ ID NO 263
LENGTH: 303
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US-08-482-785-6
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                                                                                                                           FEATURE:
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APPLICANT: Moll, Gert N.
APPLICANT: Leethouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
FILE REPERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DATE: 2003-02-07
PRIOR PAPLICATION NUMBER: EP 02077060.8
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 RQTQVSNDVVLNDGATKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGRTRTARGTLTYANVEGSYGVRQSFGKNQNPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEAA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
99.4%; Score 1213; DB 5; Length 271;
Best Local Similarity 99.1%; Pred. No. 1.4e-121;
Matches 227; Conservative 1; Mismatches 1; Indels
                  APPLICANT: Takeda, Yoshifumi
APPLICANT: Igarashi, Hisanaga
APPLICANT: Igarashi, Hisanaga
APPLICANT: Hinuma, Yorio
TITLE OF INVENTION: Mitogenic Factor, Gene Thereof and
TITLE OF INVENTION: Method of Microdetection Therefor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STRET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,721A FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: MULPAY Jr., GGFALA M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1422-178P
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-10-360-101-263
i Sequence 263, Application US/10360101
; GENERAL INFORMATION:
Kishishita, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                   ZIP: 22042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-188-721A-2
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1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 38
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                                                                                                                                                                                                           Score 202; DB 8; Length 38;
Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Adams, Craig W.
APPLICANT: Adams, Patty P.-Y.
APPLICANT: Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
TITLE OF INVENTION: Streptococcus pyogenes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 202; DB 15;
Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                           Query Match
16.6%; Score 202; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 38; Conservative 0; Mismatches
                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09119900 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 95,
TELECOMMUNICATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-terminal
 SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
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GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91001
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GENERAL INFORMATION:
APPLICANT: Broudy, Thomas B.
APPLICANT: Pancholi, Vijaykumar
APPLICANT: Pischetti, Vijaykumar
APPLICANT: Fischetti, Vincent A.
TITLE OF INVENTION: Streptococcal Genes and Gene Products
TITLE OF INVENTION: Induced by a Host Cell Contact
FILE REFERENCE: 600-1-261N
CURRENT APPLICATION NUMBER: US/09/689,278
CURRENT FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ROTOVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PALLCATION NUMBER: US/10/453,032
FILING DATE: 03-JUNE-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
16.6%; Score 202; DB 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 38; Conservative 0; Mismatches 0;
                                                                            APPLICANT: Adams, Craig W.
APPLICANT: Pang, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Peng, Party P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
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APPLICANT: Peng, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Peng, Patty P.-Y.
APPLICANT: Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, Peng, 
                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDER: US/08/082,845
APTORNEY/AGENT INFORMATION:
NAME: RAIDEN, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Sequence 6, Application US/10453032 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (818) 796-4000
(818) 795-6321
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ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                      ADDALL
STREET: 245
CITY: Pasadena
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: pept
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Query Match
Best Local Similarity 28.0%; Pred. No. 4.5e-10;
Matches 63; Conservative 37; Mismatches 80; Indels 45; Gaps 13;
                                                                                                                                                                                                                                                                                                                        92 PAGWIGNPNHVKYKIEWLNG--LSYVGDFWNRSHLIADSLGG--DALRVNAVIGIRIONV 147
                                                                                                                                                                                                                                                                                                                                              148 G---GRDOKG--GMRYTEORAQEWLEANRDGYLYYEVAPIYNADELIPRAV----- 193
                                                                                                                                                                                                                                                                          33 YYKTLGTSQITPALFPKAGDILYSKLDELGRTRTARGTLTYANVEGSYGVRQSFGK-NQN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 -----VVSMQSSDNTINEK----VLVYNTANGYTINYHNGTPTQK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 SGELLTIRLNSNKESIDENGVTTVILENSAPNINLDYLNGTATPK 251
PRIOR APPLICATION NUMBER: 60/158,772
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
LENGTH: 252
TYPE: PRT
TYPE: PRT
US-09-689-278-2
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Search completed: January 5, 2004, 18:55:07 Job time : 274.282 secs

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Minimum DB Maximum DB

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Sequence 13, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17850, A Sequence 2411, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 377, Appl Sequence 377, Appl Sequence 377, Appl Sequence 377, Appl Sequence 374, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 344, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 344, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797, Appl Sequence 1797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,630

FILING DATE: 07-Jun-1995

FILING DATE: 07-Jun-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/082,845

FILING DATE: CUNKNOWN-

ATTORNEY/AGENT INFORMATION:

NAME: Farber, Michael B.

REGISTRATION NUMBER: 32,612

REFERENCE/DOCKET NUMBER: 9521

TELECOMMUNICATION INFORMATION:

TELEPHONE: (818) 795-4301

INFORMATION FOR SEQ ID NO: 96-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Adams, Craig W.
Pang, Patty P.-Y.
Belei, Martina
TITLE OF INVENTION: Recombinant DNase B Derived from Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
                                        US-08-973-363A-17
US-10-679-063-17850
US-10-679-063-17850
US-10-425-114A-44550
PCT-US03-12256-98
US-10-272-88-7
US-10-272-88-7
US-10-272-88-6
US-10-272-89-6
US-10-272-89-6
US-10-272-89-6
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US-10-272-89-6
US-10-474-776-328
US-10-474-776-328
US-09-581-286A-477
US-09-581-286A-477
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US-09-581-286A-477
US-09-581-286A-477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1220;
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LENGTH: 229 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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    Sequence 15, Appl
Sequence 6, Appli
Sequence 16, Appl
Sequence 436, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 51758, A
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53765, A
57900, A
56379, A
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21735, A
4134, Ap
8, Appli
                                                                                                                                                    Search time 36.2689 Seconds (without alignments) 408.499 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                             1220
1 RQTQVSNDVVLNDGASKYLN......VYNTANGYTINYHNGTPTQK 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pending_Patente_AA_New:*

'cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
'cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
'cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
'cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
'cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
'cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
'cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-425-114A-47841
US-09-897-516A-6199
PCT-US03-06962-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                           320769 segs, 64697744 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                              protein search, using sw model
                                                                                                                                                      January 5, 2004, 18:39:19
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
                                                                                                                                                                                                                                         US-08-482-785-9
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Match Length
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1220 1220 1215 202 170 122.5 106 97

Result

87.5 87.5 87

86 86..5 86..5 86 86 86 86

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LGRITRIARGILIYANVEGSYGVRQSFGKNQNPAGWIGNPNHVKYKIEWLNGLSYVGDFWN 120
                                                                                                                                                                                                                                                                     Sequence 15, Application US/08472630 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            · LENGTH: 272 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228;
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Best Local S
Matches 228
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                               ö
                                                                                                                                     LGRIRIARGILIYANVEGSYGVROSFGKNONPAGWIGNPNHVKYKIEWLNGLSYVGDFWN 120
                                                                                                                                                           RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVA 180
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                                                                1 RQTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
                                                                                               ROTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDE
                               Gaps
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                                                                                                                                                                                                                                                                                                            181 PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pang, Patty P.-Y.
Belei, Marina
TITLE OF INVENTION: Recombinant DNase B Derived from
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                               0;
              Pred. No. 2.4e-96;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: «UNARNOWM>
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Uun-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 271 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08472630
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (818) 795-6321
100.08; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Pasadena
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS
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                                  229; Conservative
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Best Local Similarity
Matches 229; Conserv
              Best Local Similarity
Matches 229; Conserv
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45 QTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFFRAGDILYSKLDEL 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 GRIRTARGILIYANVEGSYGVRQSFGKNQNPAGWIGNPNHVKYKIEWLNGLSYVGDFWNR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHLIADSLGGDALRVNAVTGTRTONVGGRDOKGGMRYTEORAGEWLEANRDGYLYYEVAP 224
                                                  121 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQXGGMRYTEQRAQEWLEANRDGYLYYEVA 180
                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHILIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYYEVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QTQVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDEL
103 LGRIRTARGILITYANVEGSYGVRQSFGRNQNPAGWIGNPNHVKYKIEWINGLSYVGDFWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                        PIYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 229
                                                                                                                                                                                       Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 100.0%; Pred. No. 7.6e-96; 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Parther, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 91001
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-08-472-630-15
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Adams, Craig W.
Pang, Patty P.-Y.
Belei, Marina
TITLE OF INVENTION: Recombinant
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APPLICANT: TUTTE OF INVERSITY
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS, TREATMENT AND
TITLE OF INVENTION: PREVENTION OF ACTIVE INFECTION
FILE REPRENCE: 700355-52241-PCT
CURRENT APPLICATION NUMBER: PCT/US03/27401
CURRENT FILING DATE: 2003-09-02
PRIOR PPLIATION NUMBER: US 60/407,082
PRIOR PILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 560
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 436
LENGTH: 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 32;
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                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION: <UNFOWN>
PRIOR APPLICATION DATA:
                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
ZIP: 91001
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.0%; Score 122.5; DB 1; Best Local Similarity 22.3%; Pred. No. 0.0037; Matches 57; Conservative 34; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.9%; Score 170; DB 4; 100.0%; Pred. No. 3.8e-08; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 OTOVSNDVVLNDGASKYLNEALAWTFNDSPNY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 OTOVSNDVVLNDGASKYLNEALAWTFNDSPNY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/082,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pyogenes
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFREENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TQVSNDVVLNDGASKYLNEALAWTFND----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (818) 795-5321
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 32 amino acids
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.C
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US03-27401-436
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                                                     225 IYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 272
                         182 IYNADELIPRAVVVSMQSSDNTINEKVLVYNTANGYTINYHNGTPTQK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBALE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/472,630
FILING DATE: 07-Jun-1995
CLASSIFICATION: «Unknown»
PRIOR APPLICATION ADTR:
APPLICATION DATR:
APPLICATION DATR:
APPLICATION DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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PPLICANT: Adams, Party P.-Y.
Belei, Marina
TITLE OF INVENTION: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                        DNase B Derived from
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ROTOVSNDVVLNDGASKYLNEALAWTFNDSPNYYKTLG 38
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                                                                                                                                                                                    Sequence 6, Application US/08472630
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
APPLICANT: Adams, Patty P.-Y.
Balai, Marina
TITLE OF INVENTION: Recombinant DNase B Des
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus pyogenes
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (818) 796-4000
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LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 38, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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APPLICANT: Adams,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 SQALAESVLTDAVKSQIKGSLEWNGSGAFIVNGNKTNLDAKVSSKPYADNKTKTVGKETV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 TPALFPKAGDILYSKLDE--LGRIRTARGTLTYANVEGSYGVRQSFGKNONPAGWIGNPN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 -----ptvanallskatroyknrketgngstsw--------tptpgw---- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 HVKYKIEWLNGLSYVGDFWNRSHLIADSL----GGDALR---VNAVTGTRTONVGGRDQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 ---HQVKNLKG-SYTHAV-DRGHLLGYALIGGLDGFDASTSNPKNIAVQTAWANQAQAEY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 KGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQSSDNTINEKVLVY 211
50 SQALAESVLTDAVKSQIKGSLEWNGSGAFIVNGNKTNLDAKVSSKPYADNKTKTVGKETV 109
                                                                                                                                                                                                                153 KGGMRYTEQRAQEWLEANRDGYLYYEVAPIYNADE-LIPRAVVVSMQSSDNTINEKVLVY 211
                                                                                                                                                                                                                                                                                                                         STGQNYYESKVRKALDQNK--RVRYRVTLYYASNEDLVPSASQIEAKSSDGELEFNVLVP 255
                                                                         43 TPALFPKAGDILYSKLDE--LGRTRTARGTLTYANVEGSYGVROSFGKNONPAGWTGNPN 100
                                                                                                                                                                              101 HVKYKIEWLNGLSYVGDFWNRSHLIADSL----GGDALR---VNAVTGTRTQNVGGRDQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHIRON SPA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: PO26926WO
CURRENT APPLICATION NUMBER: US/10/472,928
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: DNA-entry nuclease (endA)
OTHER INFORMATION: Cellular location: outside
OTHER INFORMATION: Similar to strain R6 sequence 15903821 (e-156)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.0%; Score 122.5; DB 6; Length 274; Best Local Similarity 22.3%; Pred. No. 0.0037; Matches 57; Conservative 34; Mismatches 100; Indels 65.
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                                                                                                                             ----PTVANALLSKATRQYKNRKETGNGSTSW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4092, Application US/10472928
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SegWin99, version 1.03
                                                                                                                                                                                                                                                                                                                                                                                                               | | ::| | | 256 NVQKGLQLDYRTGEVT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 NTANGYTINYHNGTPT 227
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                                                                                                                                                                                                                                                                                                                                                                                  NTANGYTINYHNGTPT 227
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LENGTH: 274
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                                                                                                                                                                                                                                                                                                                                                                                  212
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; Sequence 4, Application US/08472630; GENERAL INFORMATION:

RESULT 8 US-08-472-630-4

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APPLICANT: Cao, Yongwei TTLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Dlants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114A CURRENT APPLICATION NUMBER: US/203-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 51758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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FITLE OF INVENTION: Recombinant DNase B Derived from
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                      STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 106; DB 4;
Pred. No. 0.0072;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,845
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/472,630 FILING DATE: 07-Jun-1995 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pyogenes
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 51758, Application US/10425114A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 9521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QTQVSNDVVLNDGASKYLNEALA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTOVSNOVVLNDGASXYLNEALA 23
                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (818) 796-40
TELEFAX: (818) 795-6321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 23 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.7%;
Best Local Similarity 95.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                            STATE: California
COUNTRY: USA
                                                   NUMBER OF SEQUENCES:
                                                                                                                                                       CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                             ZIP: 91001
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                                                                                                                                                                                                                                                           73 YANVEGSYGVRQSFGKNQNPAG-----WTGNPNHVKYKIEWLNGLSYVG-----DF 118
                                                                                                                                                                                                                                                                                                                                          119 WNRSHLIAD---SLGGDALRVNAVTGTRTQNVGGRDQ--KGGMRYTEQRAQEWLEANRDGY 174
                                                                                                                                                                                                                                                                                                                                                                            106 HTMKSVPADAKTMGEVMFRGNTVMNGYLKDLKATQEAFKGGWFWTGDLGVK----HPDGY 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 NGLSYVGDFWNRSHLIADSLGGDALRYNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLEA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 RSRPYLF-----SNSLAPSIVAASIKVLDMLKDGDELRERLWRNANLFREKM----T 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 NRDGYLYYEVAPIYNADELIPRAVVVSMQSSD--------NTINEKVLVYNT 213
                                                                                                                                                                              14 GASKYLNEALAWTFNDSPNYYKTL-GTSQITPALFPKAGDILYSKLDELGRTRTARGTLT 72
                                                                                                                                                                                                         6 GAPTVLNMII----NSSPKVQKPLPGKVQVMTGGAPPPDVIF-RMEELG-------50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Stater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorabdus sp. Genome Sequences And Uses Thereof FILE REFERENCE: 38-21(5.847)B
FILE REFERENCE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34;
                                                                                               8.0%; Score 97; DB 6; Length 281;
ilarity 23.2%; Pred. No. 0.55;
Conservative 39; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.4%; Score 90; DB 5; Length 398; Best Local Similarity 24.6%; Pred. No. 3.1; Matches 31; Conservative 18; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 LYYEVAPIYNADELIPRA--VVVSMQSSDNTINEKVLVYN 212
                                   ; OTHER INFORMATION: Clone ID: 700869544_FLI.pep
US-10-425-114A-51758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6933, Application US/09897516A
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21735, Application US/10679063
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 8415
SEQ ID NO 6933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Xenorhabdus sp.
                                                                                 Query Match
Best Local Similarity
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |:|:
AAGFTL 320
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US-10-679-063-21735
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TGNPNHVKYKIEWLNGLSYVGDFWNRSHL-----IADSL------GGDALRVN 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 VIAVDQNTSPVÄRPVTPVGDQQVWGT---KNADGSYTV-ALFNLGDSPÄSVTAHWASFGF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 AVTGTRTQ------NVGGRD----QKGGMRYTEQRAQ-EWLEANRDGYLYYEVAP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----RTRTAR-----GTLTYANVEGSYGVRQSFGKNONPA------GW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 DGASKYLNEA--LAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELG-----
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APPLICANT: WRIGHT, Rachel J; BRUNS, Christopher M;
APPLICANT: WRIGHT, Rachel J; BRUNS, Christopher M;
APPLICANT: MARJANOVIC, Mirjana M; SHEN, Fan;
APPLICANT: MARTSHORNE, Toinette A; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M; PITTS, Steven J;
APPLICANT: BLOBE, Linda V; MOONEY, Elizabeth M;
APPLICANT: BANYLLE, Steven C; REDDY, Thirupathi P;
APPLICANT: STEVENS, Kristian A; BLANCHARD, John L;
APPLICANT: PARZER, SCOOT R; WANG, Xinhao;
APPLICANT: PERALTA, Careyna H; ANDERSON, SCOT E;
APPLICANT: PERALTA, Careyna H; ANDERSON, SCOT E;
APPLICANT: WU, Mingham C; STUVE, Laura L;
APPLICANT: WU, Mingham C; STUVE, Laura L;
APPLICANT: VITT, Ursula A; KIRTO, Peter A;
APPLICANT: VITT, Ursula A; KIRTO, Eter A;
APPLICANT: VITT, Ursula A; KIRTO, Eter A;
APPLICANT: VITT, Ursula A; KIRTO, Eter A;
APPLICANT: WU, Mingham C; STUVE, Laura L;
APPLICANT: STEWART, Elizabeth A; WINGROVE, James A;
APPLICANT: STEWART, Elizabeth A; WINGROVE, James A;
APPLICANT: WITH AND ANDERCULES BONNIE L;
APPLICANT: WITH AND ACKSON, Jennifer L;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
TITLE OF INVENTION: WOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60; Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 608;
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 87.5; DB 6; ilarity 24.4%; Pred. No. 7.9; Conservative 25; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptomyces avermitilis MA-4680 US-10-679-063-21735
                          FILE REFERENCE: 38-15 (22054) B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
ERG ID NO 21735
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CURRENT APPLICATION NUMBER: PCT/US03/28227
CURRENT FILING DATE: 2003-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 4134, Application PC/TUS0328227 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
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Best Local Similarity
Matches 64; Conservat
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; OTHER INFORMATION: Description of Artificial Sequence: Hybrid of Group A Streptococc; OTHER INFORMATION: protein and M-like protein
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Dants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 GMRYTEQRAQEWLE-----ANRDGYLYYEVAPIY-----NADELIPRAVVVSMQSSDNTI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 --KIEWLNGLSYVGDFWNRSHLIADSLGG------DALRVNAVTGTRTQNVGGRDQKG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 GASKYLNEALAW-TFNDS------PNYYKTLGTSQITPALFPKAGDILYSKLDELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 KLRDEYYTLIDAKEEEPRYKALGTLLDQVTQLYTKH-----NSNYQQYNAQAGRLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 RIRTARGILIYANVE-----GSY--GVRQSFGKNONPAGWIGNPNHVKY-----
                                                                                                                                                                                                                                            APPLICANT: University of Tennessee Research Corporation
APPLICANT: University of Tennessee Research Corporation
APPLICANT: Reddish, Mark A.
APPLICANT: Hu, Mary C.
APPLICANT: Walls, Michael A.
APPLICANT: Walls, Michael A.
APPLICANT: Dale, James B.
TITLE OF INVENTION: MULTIVALENT STREPTOCOCCAL VACCINE COMPOSITIONS AND
TITLE OF INVENTION: METHODS FOR USE
FILE REFERENCE: 481112.413PC
CURRENT APPLICATION NUMBER: PCT/US02/34769
CURRENT PILING DATE: 2003-05-19
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Gaps
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                                                                                                                                                                                                                                      APPLICANT: ID Biomedical Corporation of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 53765, Application US/10425114A; GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                             Sequence 16, Application PC/TUS0234769
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 NEKVL 209
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205 NEKVL 209
                                                 351 ENKKL 355
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US-10-425-114A-53765
                                                                                                                                                         PCT-US02-34769-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 ROKAEYLKGLN----DWAER----LLQELNGTNNDGRSRDVTEEIAANNTTVQNIRLRNENK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 GMRYTEQRAQEWLE-----ANRDGYLYYEVAPIY-----NADELIPRAVVVSMQSSDNTI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LGRIRIARGTLTYANVEGSYGVRQSFGKNONPAGWTGNPNHVKYKIEWLNGLSYVGDFWN 120
                                                                                                                                                                                                                                                                                                                                                                                                        282 IGRKGATGATTIYAVEADGDPNAGFEKNK-----EPGEIQYLIKW-KGWSHIHNTWE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 RSHLIADSLGGDALRVNAVTGTRTQNVGGRDQKGGMRYTEQRAQEWLE-ANRDGYLYYE- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 --KIEWLNGLSYVGDFWNRSHLIADSLGG------DALRVNAVTGTRTQNVGGRDQKG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: University of Tennessee Research Corporation
APPLICANT: University of Tennessee Research Corporation
APPLICANT: Reddish, Mark A.
APPLICANT: Reddish, Mark A.
APPLICANT: Walls, Michael A.
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TITLE OF INVENTION: METHODS FOR USE
FILE REFERENCE: 481112.413PC
CURRENT APPLICATION NUMBER: PCT/US02/34769
CURRENT APPLICATION NUMBER: PCT/US02/34769
CURRENT FILING DATE: 2003-05-19
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.1
SEG ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GASKYINEALAW-TFNDS------PNYYKTLGTSQITPALFPKAGDILYSKLDELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 RIRTARGILIYANVE-----GSY--GVROSFGKNONPAGWIGNPNHVKY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                  Length 1738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 7.1%; Score 87; DB 1; Length 428; Local Similarity 24.5%; Pred. No. 6; hes 60; Conservative 32; Mismatches 89; Indele
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                         ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 957668.PTlp
PCT-US03-28227-4134
                                                                                                                                                                                                                                                                  7.2%; Score 87.5; D 20.5%; Pred. No. 23; Live 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 QQELTDDLHKQYQIVERIIAHSNQKS 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 ----VAPIYNADELIPRAVVVSMQSS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US02-34769-8
; Sequence 8, Application PC/TUS0234769
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                         30; Conservative
                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 TEETL-----
     SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 30; Conserve
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                                SEQ ID NO 4134
LENGTH: 1738
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Best Local S:
Matches 60
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                                                                                                                                         FEATURE
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                                                                                                                                                                                                                                                                             136 VNAVIGTRION------VGGRDQ-----KGGMRYTEQRAQEWLEANRDGYLYYEVA 180
                                                                                                                                                                                                                        8 DVVLNDGASK----YLNEALAWTFNDSPNYYKTLGTSQITPALFPKAGDILYSKLDELG- 62
                                                                                                                                                                  Query Match
7.1%; Score 86.5; DB 6; Length 331;
Best Local Similarity 20.1%; Pred. No. 5.1;
Matches 58; Conservative 36; Mismatches 88; Indels 107; Gaps
                                                                                                                                                                                                                                                                                                                                                                                         181 PIYNADELIPRAV-VVSMQSSDNTINEKVLVYNT----ANGYTINYHNG 224
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73033D04_FLI.pep
US-10-425-114A-53765
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